

RESULT 2

US-09-439-313-527

; Sequence 527, Application US/09439313

; PATENT NO. 6328505

; GENERAL INFORMATION:

; APPLICANT: XU, Jiangchun

; APPLICANT: Billon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlacher, Susan Louise

; APPLICANT: Jiang, Yuqui

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Rettner, Mark

; APPLICANT: Salk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND FILE REFERENCE: 210121-427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 527

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-439-313-527

Query Match 60.6%; Score 983; DB 4; Length 320; Best Local Similarity 59.8%; Pred. No. 8.9e-83; Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

Qy 8 NESSATYFLIGLIGPLRQAQMLAFLPCLPSLYLAVIGNLTIVYVREHSLHEPMYFLC 67

Db 5. NEFHAT-FVLIGIGPLERKHNFWGFPPLSMYVVMFGNCIVVFLVTERSLHAPMFLFC 63

Qy 68 MLESGIDILISTSSMPKMLAIFENNSTIQQFDACIQLQMAHSLSGESTVLLAMAFLDRV 127

Db 64 MLAADIALSTSMKPLKLAFLFEDSREIACLTOMFTHALSAESTTLLAMAFLDRV 123

Qy 128 ALCHPLRHLRHTAVLFLPRTKIGAVAVRGAALMAPLPYFKIQKOLPFCRSNLISHSYCLHDQV 187

Db 124 ALCHPLRHLRHTAVLFLPRTKIGAVAVRGAALMAPLPYFKIQKOLPFCRSNLISHSYCLHDQV 183

Qy 188 MKLACADDIIRRNVYGLIVTISAGLDSLISSEYLLIKTIVGL-TREBQAKAFGTCVSH 246

Db 184 MKLAYADLPLNVIGLTAILLYMGVDMFISLYSFLIRTQLPSKSERAKAFGTCVSH 243

Qy 247 VCAVETIPTWPFGLSMYHFRFSRDRSPFLVILANITYLWPPVNPVYVGKMKIEIRQL 306

Db 244 IGVLAFLPTVPLIGLSVHFGNSLHPTVVRVMDIVLILPPVNPVNPVYGAKTQIRTRVL 303

RESULT 4

US-09-053-303-2

Sequence 2, Application US/08465980

; Patent No. 5756309

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Li, Yi

; APPLICANT: Rosen, Craig A.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,980

; FILING DATE: 06 JUN 1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 36,134

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1744

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 320 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-465-980-2

Query Match 59.7%; Score 968.5; DB 1; Length 320; Best Local Similarity 59.7%; Pred. No. 1.9e-81; Matches 178; Conservative 53; Mismatches 66; Indels 1; Gaps 1;

Qy 16 TLIGIGPLERKHNFWGFPPLSMYVVMFGNCIVVFLVTERSLHAPMFLFC 75

Db 12 VLIGIGPLERKHNFWGFPPLSMYVVMFGNCIVVFLVTERSLHAPMFLFC 71

Qy 76 ISTSSMPKMLAIFENNSTIQQFDACIQLQMAHSLSGESTVLLAMAFLDRV 137

Db 72 LSTSSMPKMLAFLFEDSREIACLTOMFTHALSAESTTLLAMAFLDRV 131

Qy 136 ATVILFLPRTKIGAVAVRGAALMAPLPYFKIQKOLPFCRSNLISHSYCLHDQV 195

Db 132 AAVINNTVYQIGIVAVVWSLSEFLPPLIKLAFCHSNLISHSYCLHDQV 191

Qy 196 RVNVYGLIVTISAGLDSLISSEYLLIKTIVGL-TREBQAKAFGTCVSHVCAVFLY 254

Db 192 LPNWTGFLAILLYMGVDMFISLYSFLIRTQLPSKSERAKAFGTCVSH 251

Qy 255 VPFGLSMYHFRFSRDRSPFLVILANITYLWPPVNPVYVGKMKIEIRQL 312

Db 252 VPLIGLGSVHFGNSLHPTVVRVMDIVLILPPVNPVNPVYGAKTQIRTRVL 309

Qy 307 RLHVA 312

; :: :

QY 307 RLEFVA 312
Db 304 AMFKIS 309

RESULT 3

RESULT 4
US-09-053-303-2
; Sequence 2, Application US/09053
; Patent No. 5948990
; GENERAL INFORMATION:
; APPICANT: Soppet, Daniel R.

APPLICANT: Li, YI
 APPLICANT: Rosen, Craig A.
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/053, 303
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-446
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 320 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-053-303-2

Query Match 59.7%; Score 968.5; DB 2; Length 320;
 Best Local Similarity 59.7%; Pred. No. 1.9e-81; Gaps 1;
 Matches 178; Conservative 53; Mismatches 66; Indels 1; Gaps 1;

Qy 16 ILIGGLPGLEADPLAFLPCLSILIAVGNLTIIYIVTEHSHHEPMYFLCMGSGIDL 75
 Db 12 VLIGIGPLEKAMHFWGEPFLSMVWAMCGCIVTVFVRRERSHAPMFLCMLAIDIA 71
 Qy 76 ISTSSPKMLAIFENNSTIOTFDACLQFLNFAIRSLGMSMESTVILAMARFRYVATCPLR 135
 Db 72 LSTSTPKMLAFLWEDSREISIACLTQFLNFAIRSLAISTVILAMAFRDYVATCPLR 131
 Qy 136 ATVLLPRTKIGVAVVRGAALMAPLVPFLKQFLPFCNSNLSHSCYHODVWKLACDDI 195
 Db 132 AAVLNTVTAQIGIVAVGSLFEPFLPLKLAFCNSHNLSHSCYHODVWKLACDDI 191
 Qy 196 RVWVGLTVAISAGLDSLISFSYSLITKTLGGL-TREAQKAFGCVSHCAVFLY 254
 Db 192 LPNVVYGLTALLVMGVDFMFLISYFLIRTQVLPKSKERAKAFGCVSHCVLAFF 251
 Qy 255 VPEIGLSMWHRSKRSRDKSPFLPVILANTVILVPPVLPNTYGVKKEIRQRLRPHVA 312
 Db 252 VPLIGLSVWHRFGNSLHPIVVMGDIYLILPPVNPVNPVYGAQTKQIRTRVLMFKS 309

RESULT 5
 US-09-339-115-2
 Sequence 2, Application US/09339115
 Patient No: 637891
 GENERAL INFORMATION
 APPLICANT: Soppet, Daniel R.
 APPLICANT: Li, YI
 APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
 NUMBER OF SEQUENCES: 8

RESULT 6
 PCT-US95-07093-2
 Sequence 2, Application PC/ATUS9507093
 GENERAL INFORMATION:
 APPLICANT: Soppet, Daniel R.
 APPLICANT: Li, YI
 APPLICANT: Rosen, Craig A.
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
 NUMBER OF SEQUENCES: 8

APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/339, 115
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-446
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 320 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-339-115-2

Query Match 59.7%; Score 968.5; DB 4; Length 320;
 Best Local Similarity 59.7%; Pred. No. 1.9e-81; Gaps 1;
 Matches 178; Conservative 53; Mismatches 66; Indels 1; Gaps 1;

Qy 16 ILIGGLPGLAOFWAPLPSILIAVGNLTIIYIVTEHSHHEPMYFLCMGSGIDL 75
 Db 12 VLIGIGPLEKAMHFWGEPFLSMVWAMCGCIVTVFVRRERSHAPMFLCMLAIDIA 71
 Qy 76 ISTSSPKMLAIFENNSTIOTFDACLQFLNFAIRSLGMSMESTVILAMARFRYVATCPLR 135
 Db 72 LSTSTPKMLAFLWEDSREISIACLTQFLNFAIRSLAISTVILAMAFRDYVATCPLR 131
 Qy 136 ATVLLPRTKIGVAVVRGAALMAPLVPFLKQFLPFCNSNLSHSCYHODVWKLACDDI 195
 Db 132 AAVLNTVTAQIGIVAVGSLFEPFLPLKLAFCNSHNLSHSCYHODVWKLACDDI 191
 Qy 196 RVWVGLTVAISAGLDSLISFSYSLITKTLGGL-TREAQKAFGCVSHCAVFLY 254
 Db 192 LPNVVYGLTALLVMGVDFMFLISYFLIRTQVLPKSKERAKAFGCVSHCVLAFF 251
 Qy 255 VPEIGLSMWHRSKRSRDKSPFLPVILANTVILVPPVLPNTYGVKKEIRQRLRPHVA 312
 Db 252 VPLIGLSVWHRFGNSLHPIVVMGDIYLILPPVNPVNPVYGAQTKQIRTRVLMFKS 309

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GIFFILLAN, CECCHI,
 ADDRESSEE: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07093

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/465,980

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 3325800-446

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: protein

Query Match 59.7%; Score 968.5; DB 5; Length 320;
 Best Local Similarity 59.7%; Pred. No. 1.9e-81; Indels 1; Gaps 1;

Matches 178; Conservative 53; Mismatches 66; Indels 1; Gaps 1;

QY 16 IIGLGPQLEAQFQLAPLCSILYIAVLGNITIIVRTEHSLHEPMYIFCMLSGSDIL 75

Db 12 VLGIGPQLEKHFVWQGPPLSMVVMCGNCIVVFTVTERSLHAPMFLICMLAIDL 71

Qy 76 ISTSSPERMLAIFWENSTTDFACIQLQMPATHSISGMSSTVLLAMAIFDRYVACIPLRH 135

Db 72 ISTMSPKILAFWEDSREIESTACIQLQMPATHSISVLLAMAIFDRYVACIPLRH 131

Qy 136 ATWLTLPFRVIGVAAVRGALMAPLVEKOLPPCRSNLISLHSYCLHQDMVAKLACDD 195

Db 132 AAVLNNVNTTAIGIVAVRGLFFPLPLIKRFLAFCHSNLTHSPYCVHODYVMLKLVADT 191

Qy 196 RYNNVYGLIVIVISAGLDSLISFSYLITKTVGL-TREQAQKAGTGTCSVHCAVIFY 254

Db 192 LPNWVIGLTAILLVMGVDMVFLISLSPKSKERAKAGTCVSHIGVLAFY 251

Qy 255 VPIFIGLSMWHFNSKRDSPVPLVANIYLVPPVLPPIVGVKTEIRORTLRLFVA 312

Db 252 VPIGLISVVRGPNLHPIVVRVWMDIVLILAPPVNPVNPVIVGVK 297

RESULT 7
 US-08-988-876-7
 Sequence 7, Application US/08988876
 Patent No. 6063596
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED WITH IMMUNE RESPONSE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:

ADDRESSEE:

Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,876

FILING DATE: Herewith

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 314 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 32086

US-08-988-876-7

Query Match 26.6%; Score 431.5; DB 3; Length 314;

Best Local Similarity 33.8%; Pred. No. 3.8e-32; Indels 120; Gaps 8;

Matches 109; Conservative 63; Mismatches 21; Indels 21; Gaps 8;

Qy 8 NESSATYFLIGLIGPLEERQFIALPFLCSILYIAVLGNITIIVRVERHSLEHPMYIFLC 67

Db 5 NQPSISDFLILGQIOPCQNCYALEFLAMYLUTLNLNLILTVLRLDHLTHPMLFLPS 64

Qy 68 MUSGIDILSTTSMPKMLAIFWENSTTDFACIQLQMPATHSISVLLAMAIFDRYVACIPLRH 127

Db 65 NLFSFSDLCFESSVTPKLIQNMQDPSIYADCLTOMFPLLEGDLSPFLYAMAVRY 124

Qy 128 ATCHPLRPLATVLTLPFRVIGVA---AVTRGALMAPLVPFVKOLPPCRSNLTHSPC 184

Db 125 AJCPPL-RTMAMSPMCLALVALSWLTFHAMHTL--LMARLCFCADNVPHFCDDM 181

Qy 185 QDMKLAQCDIRN---WVGLIVIVISAGLDSLISFSYLISVLLILTVLTVGL-TREQAQ 238

Db 182 SALKLAKFSDTRNEWWIFIMGGILVW---PFLIGLGSYARIIVSILKVPSSKICK 236

Qy 239 AFGTCVSIVCAVPIFYVPIFGLSVHFRSSRROSPL-PVILANIYLVPPVNPVPIVGVK 297

Db 237 AFSTCGSHLSWSLFIGVIVGLC---SSANSTLKDVTMAMMTVTPMUNPPIYSLR 293

Qy 298 TKEIIRORTLRLFH 310

Db 294 NRDMKGALSRVH 306

RESULT 8
 US-08-988-876-5
 Sequence 5, Application US/08988876
 Patent No. 6063596
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED WITH IMMUNE RESPONSE

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

Query Match 24.6%; Score 398.5; DB 3; Length 309; Best Local Similarity 29.3%; Pred. No. 4e-29; Matches 88; Conservative 75; Mismatches 126; Indels 11; Gaps 5;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

Query Match 23.4%; Score 380; DB 3; Length 333; Best Local Similarity 28.0%; Pred. No. 2.2e-27; Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

APPLICANT: Lal, Preetai
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED WITH IMMUNE RESPONSE

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0441 US

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith

RESULT 9
 US-08-988-876-6
 ; Sequence 6, Application US/08988876
 ; Patent No. 606396
 ; GENERAL INFORMATION:

RESULT 10

US-08-467-948A-2

Sequence 2, Application US/08467948A

; Patent No. 5998164

; GENERAL INFORMATION:

; APPLICANT: LI, YI

; APPLICANT: CAO, LIANG

; APPLICANT: NI, JIAN

; APPLICANT: GENTZ, REINER

; APPLICANT: BULT, CAROL J.

; APPLICANT: SUTTON III, GRANGER G.

; APPLICANT: ROSEN, CRAIG A.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STEER, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PATENT RELEASE #1.0, VERSION #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467, 948A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04079

; FILING DATE: 30-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 296 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-467-948A-2

Query Match 22.6%; Score 367; DB 2; Length 296; Best Local Similarity 32.2%; Pred. No. 3e-26; Matches 94; Conservative 61; Mismatches 121; Indels 16; Gaps 7;

; Query Match 22.6%; Score 367; DB 3; Length 296; Best Local Similarity 32.2%; Pred. No. 3e-26; Matches 94; Conservative 61; Mismatches 121; Indels 16; Gaps 7;

; QY 8 NESSATYFILGL--PGLEBAQFLAFCPLSL-YIAVIGNLTIVYVTEHSLHEPMY 63

; DB 8 NOTMVFTEFLIGFLIGPQI--MILFGFLSLFVFTLIGNTLGLISDRHTPMY 63

; QY 64 IFICLMSGIDLILSTSSMPMLAIFWFNSTIQTIDACIQLQFATHSLSGMESTVLLAMAP 123

; DB 64 FELSHLAVVNVAYCNTVPMVLNLHLPKAPISFGCMTDFLFSFATPECLIVMSY 123

; QY 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; DB 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; QY 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; DB 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; QY 184 RQDVKLACDIDRIVN--WVGLIVVISAQGLSLLISFSSL--IITKVIGLTBAQAA 239

; DB 184 ILSVLVRLLACDADTWLQVWVIFEAChPLVGPCLLVLVSYSHLGLRIOSS--EGRKKA 240

; QY 240 FGTCYSHVCAVFIYVPIGLSMWVRFPSKRDSPLPVILANIVLIVPPVLP 291

; DB 241 FSTCSHICVYGLFGSGATVWYMAPK-SRNPEDDKVLFILQIPLSTPMK 291

RESULT 11

US-08-467-947A-2

Sequence 2, Application US/08467947A

; Patent No. 6090575

; GENERAL INFORMATION:

; APPLICANT: LI, YI

; APPLICANT: CAO, LIANG

; APPLICANT: NI, JIAN

; APPLICANT: GENTZ, REINER

; APPLICANT: BULT, CAROL J.

; APPLICANT: SUTTON III, GRANGER G.

; APPLICANT: ROSEN, CRAIG A.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STEER, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PATENT RELEASE #1.0, VERSION #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467, 947A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04079

; FILING DATE: 30-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 296 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-467-947A-2

Query Match 22.6%; Score 367; DB 3; Length 296; Best Local Similarity 32.2%; Pred. No. 3e-26; Matches 94; Conservative 61; Mismatches 121; Indels 16; Gaps 7;

; Query Match 22.6%; Score 367; DB 3; Length 296; Best Local Similarity 32.2%; Pred. No. 3e-26; Matches 94; Conservative 61; Mismatches 121; Indels 16; Gaps 7;

; QY 8 NESSATYFILGL--PGLEBAQFLAFCPLSL-YIAVIGNLTIVYVTEHSLHEPMY 63

; DB 8 NOTMVFTEFLIGFLIGPQI--MILFGFLSLFVFTLIGNTLGLISDRHTPMY 63

; QY 64 IFICLMSGIDLILSTSSMPMLAIFWFNSTIQTIDACIQLQFATHSLSGMESTVLLAMAP 123

; DB 64 FELSHLAVVNVAYCNTVPMVLNLHLPKAPISFGCMTDFLFSFATPECLIVMSY 123

; QY 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; DB 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; QY 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; DB 124 DRYVAIChPLRHAIVTLPLRVTKIGVAVVRGAALMAPLFVTKIQLPFCNSNLSHSYCL 183

; QY 184 RQDVKLACDIDRIVN--WVGLIVVISAQGLSLLISFSSL--IITKVIGLTBAQAA 239

; DB 184 ILSVLVRLLACDADTWLQVWVIFEAChPLVGPCLLVLVSYSHLGLRIOSS--EGRKKA 240

; QY 240 FGTCYSHVCAVFIYVPIGLSMWVRFPSKRDSPLPVILANIVLIVPPVLP 291

; DB 241 FSTCSHICVYGLFGSGATVWYMAPK-SRNPEDDKVLFILQIPLSTPMK 291

Sequence 3, Application US/09339115
 Patient No. 6377891

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R.

APPLICANT: Li, Yi

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

ADDRESSEE: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/339,115

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/053,303

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-446

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

TELEFAX: 201-994-1700

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-339-115-3

Query Match 22.3%; Score 361.5; DB 4; Length 247;
 Best Local Similarity 36.9%; Pred. No. 7.7e-26; Gaps 6;
 Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

QY 15 FILIGLPGLEEAQFWLAFLPCISLYIAVIGNLTIVIYVTEHSLHEPMWIFLCMLSGID 74

QY 1 FILIGLPGLEEAQFWLAFLPCISLYIAVIGNLTIVIYVTEHSLHEPMWIFLCMLSGID 60

QY 75 LISTSSMMRMLAFWENSTTIOFDACLICMFAHTHSLSGMESTVLLAMAADFDRVIAICHLR 134

Db 61 CFSSEVTIPKLLQNMQNDPSIYADCIQTMFFLFGDLESILVAMAYDRYVAICPL- 119

Db 135 HATVLTLLRVTKGVA--AVYRGAAALMAPLPIVFIKQPFCSNLSHYSYCHDVKLA 191

Db 120 HYAIAIMSPMCLQALVALSWWLTIFHAMHLT-LMARLFCADNVPHEFCDSMALLKA 177

QY 192 CDDIRVN---WVGLLIVLISAGLDSLISFSYLLIKVGL-TREAQAKAFGTCVS 245

QY 178 FSDTRVNEWWIFMIGGLIVI---PFLILGSYARIVSSILKVPSSKGICKAFSTCGS 232

QY 246 HVCAYEFLVYPFGL 260

Db 233 HLSVVSLSFGTVGL 247

Search completed: March 26, 2003, 09:58:02
 Job time : 29 secs

RESULT 15
 PCR-US95-07093-3
 Sequence 3, Application PC/TU95/07093

Query Match 100.0%; Score 1623; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.5e-147; Indels 0; Gaps 0;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMDVDPNGNESSATVFLIGLPGLEAQFWMLAPICSLYLVAVLGNLTIVYRTEHSLHE 60
 Db 1 MMDVDPNGNESSATVFLIGLPGLEAQFWMLAPICSLYLVAVLGNLTIVYRTEHSLHE 60

QY 61 PMXITCMLMSGIDILISTSSPMKLAIFWENSTTIOFDACLIQMAHSLSGMESTVLLA 120
 Db 61 PMXITCMLMSGIDILISTSSPMKLAIFWENSTTIOFDACLIQMAHSLSGMESTVLLA 120

QY 121 MAFDVKVVALCHPLRATVTLPRTKIGAVAVRGRALMAPLPIKOLPPCRSNLHS 180
 Db 121 MAFDVKVVALCHPLRATVTLPRTKIGAVAVRGRALMAPLPIKOLPPCRSNLHS 180

QY 181 YCLHDYDMKLAICADDIRNVYGLVIVISAGLDSLISFSYLLIKTVGLTREAOAKAF 240
 Db 181 YCLHDYDMKLAICADDIRNVYGLVIVISAGLDSLISFSYLLIKTVGLTREAOAKAF 240

QY 241 GTCVSHVCAVFLFVPPIGLSVHRSKRSRSPPLPVLYNLYLVPVLPNPIVYGVTK 300
 Db 241 GTCVSHVCAVFLFVPPIGLSVHRSKRSRSPPLPVLYNLYLVPVLPNPIVYGVTK 300

QY 301 IQRILRLFHVTHASEP 318
 Db 301 IQRILRLFHVTHASEP 318

RESULT 2
 US-09-895-793-920
 ; Sequence 920, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocke, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Rettter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Repler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.534C2
 ; CURRENT APPLICATION NUMBER: US/09/895,793
 ; CURRENT FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 990
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 920
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-895-793-920

Query Match 100.0%; Score 1623; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.5e-147; Indels 0; Gaps 0;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMDVDPNGNESSATVFLIGLPGLEAQFWMLAPICSLYLVAVLGNLTIVYRTEHSLHE 60
 Db 1 MMDVDPNGNESSATVFLIGLPGLEAQFWMLAPICSLYLVAVLGNLTIVYRTEHSLHE 60

QY 61 PMXITCMLMSGIDILISTSSPMKLAIFWENSTTIOFDACLIQMAHSLSGMESTVLLA 120
 Db 61 PMXITCMLMSGIDILISTSSPMKLAIFWENSTTIOFDACLIQMAHSLSGMESTVLLA 120

QY 121 MAFDVKVVALCHPLRATVTLPRTKIGAVAVRGRALMAPLPIKOLPPCRSNLHS 180
 Db 121 MAFDVKVVALCHPLRATVTLPRTKIGAVAVRGRALMAPLPIKOLPPCRSNLHS 180

QY 181 YCLHDYDMKLAICADDIRNVYGLVIVISAGLDSLISFSYLLIKTVGLTREAOAKAF 240
 Db 181 YCLHDYDMKLAICADDIRNVYGLVIVISAGLDSLISFSYLLIKTVGLTREAOAKAF 240

QY 241 GTCVSHVCAVFLFVPPIGLSVHRSKRSRSPPLPVLYNLYLVPVLPNPIVYGVTK 300
 Db 241 GTCVSHVCAVFLFVPPIGLSVHRSKRSRSPPLPVLYNLYLVPVLPNPIVYGVTK 300

QY 301 IQRILRLFHVTHASEP 318
 Db 301 IQRILRLFHVTHASEP 318

RESULT 3
 US-09-895-814-920
 ; Sequence 920, Application US/09895814
 ; Publication No. US20020193296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocke, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Rettter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Repler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C25
 ; CURRENT APPLICATION NUMBER: US/09/895,814
 ; CURRENT FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 990
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 920
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-895-814-920

Query Match 100.0%; Score 1623; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.5e-147; Indels 0; Gaps 0;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMDVDPNGNESSATVFLIGLPGLEAQFWMLAPICSLYLVAVLGNLTIVYRTEHSLHE 60
 Db 1 MMDVDPNGNESSATVFLIGLPGLEAQFWMLAPICSLYLVAVLGNLTIVYRTEHSLHE 60

QY 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 Db 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 QY 121 MAFDRYVAVCHPLRHATVLTLPKIGVAAVRGAALMAPLPFIKOPFCRNLHS 180
 Db 121 MAFDRYVAVCHPLRHATVLTLPKIGVAAVRGAALMAPLPFIKOPFCRNLHS 180
 QY 181 YCHQDVMKLAACDDIRVNVYGLIVISAGLDSLTSFSYLLIKTWTGIGTREQAQAF 240
 Db 181 YCHQDVMKLAACDDIRVNVYGLIVISAGLDSLTSFSYLLIKTWTGIGTREQAQAF 240
 QY 241 GTCVSHVCVAFIVYPFGLSMVRFSKRDSPLPVILANIYLVPPVNPIVYGKTE 300
 Db 241 GTCVSHVCVAFIVYPFGLSMVRFSKRDSPLPVILANIYLVPPVNPIVYGKTE 300
 QY 301 IQRIRLRLHVTHASEP 318
 Db 301 IQRIRLRLHVTHASEP 318

RESULT 4
 US-09-966-459a-2
 ; Sequence 2, Application US/09966459A
 ; Publication No. US20030022237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FEDER, J. N.
 ; APPLICANT: MINIER, G.
 ; APPLICANT: RAMANATHAN, C. S.
 ; APPLICANT: HAWKEN, D. R.
 ; APPLICANT: CAGCIC, A.
 ; APPLICANT: BARBER, L.
 ; APPLICANT: KORNACKER, M. G.
 ; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM4,
 ; TITLE OF INVENTION: EXPRESSED HIGHLY IN PROSTATE, COLON, AND LONG
 ; FILE REFERENCE: D0039NP
 ; CURRENT APPLICATION NUMBER: US/09/966,459A
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/2735,833
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/261,776
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: 60/305,351
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 60/313,202
 ; PRIOR FILING DATE: 2001-08-17
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-966-459a-2

Query Match 100.0%; Score 1623; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17; Mismatches 0; Gaps 0;
 Matches 318; Conservative 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLIGPLGLGEEAQWLAFFPLCSXLIAVGNLTITYTTERSHLE 60
 Db 1 MMVDPNGNESSATYFLIGPLGLGEEAQWLAFFPLCSXLIAVGNLTITYTTERSHLE 60
 QY 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 Db 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 QY 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 Db 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 QY 121 MAFDRYVAVCHPLRHATVLTLPKIGVAAVRGAALMAPLPFIKOPFCRNLHS 180
 Db 121 MAFDRYVAVCHPLRHATVLTLPKIGVAAVRGAALMAPLPFIKOPFCRNLHS 180
 QY 181 YCHQDVMKLAACDDIRVNVYGLIVISAGLDSLTSFSYLLIKTWTGIGTREQAQAF 240
 Db 181 YCHQDVMKLAACDDIRVNVYGLIVISAGLDSLTSFSYLLIKTWTGIGTREQAQAF 240
 QY 241 GTCVSHVCVAFIVYPFGLSMVRFSKRDSPLPVILANIYLVPPVNPIVYGKTE 300
 Db 241 GTCVSHVCVAFIVYPFGLSMVRFSKRDSPLPVILANIYLVPPVNPIVYGKTE 300
 QY 301 IQRIRLRLHVTHASEP 318
 Db 301 IQRIRLRLHVTHASEP 318

RESULT 5
 US-09-759-143-920
 ; Sequence 920, Application US/09759143
 ; Patent No. US20030022248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlock, Susan L.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stork, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedick, Thomas S.
 ; APPLICANT: Carter, Barrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeky, Yasir A.W.
 ; APPLICANT: Reper, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.42C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 920
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-759-143-920

Query Match 100.0%; Score 1623; DB 10; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.5e-147; Mismatches 0; Gaps 0;
 Matches 318; Conservative 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLIGPLGLGEEAQWLAFFPLCSXLIAVGNLTITYTTERSHLE 60
 Db 1 MMVDPNGNESSATYFLIGPLGLGEEAQWLAFFPLCSXLIAVGNLTITYTTERSHLE 60
 QY 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 Db 61 PMYIFLCLMSGIDLISTSSMPKMLAIFWENSTIQFDACLLQPAIHSLSGESTVLLA 120
 QY 121 MAFDRYVAVCHPLRHATVLTLPKIGVAAVRGAALMAPLPFIKOPFCRNLHS 180
 Db 121 MAFDRYVAVCHPLRHATVLTLPKIGVAAVRGAALMAPLPFIKOPFCRNLHS 180
 QY 181 YCHQDVMKLAACDDIRVNVYGLIVISAGLDSLTSFSYLLIKTWTGIGTREQAQAF 240
 Db 181 YCHQDVMKLAACDDIRVNVYGLIVISAGLDSLTSFSYLLIKTWTGIGTREQAQAF 240
 QY 241 GTCVSHVCVAFIVYPFGLSMVRFSKRDSPLPVILANIYLVPPVNPIVYGKTE 300
 Db 241 GTCVSHVCVAFIVYPFGLSMVRFSKRDSPLPVILANIYLVPPVNPIVYGKTE 300
 QY 301 IQRIRLRLHVTHASEP 318
 Db 301 IQRIRLRLHVTHASEP 318

RESULT 6
US-09-780-669-920
; Sequence 920, Application US/09780669

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Repler, John
; APPLICANT: Rural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-622-627-920
Query Match 100.0%; score 1623; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147; Mismatches 0; Indels 0; Gaps 0;
Matches 318; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
Oy 1 MMYDPNGNESSATYFILIGPGLQEEQFWAPLPCSLXLAUGNLTIIYVTERHSHE 60
Db 1 MMYDPNGNESSATYFILIGPGLQEEQFWAPLPCSLXLAUGNLTIIYVTERHSHE 60
Oy 61 PMYFLCMLSGIDILSTSMPRMLATFWENSTTIGDACLQMFATHSLSGMESTVLLA 120
Db 61 PMYFLCMLSGIDILSTSMPRMLATFWENSTTIGDACLQMFATHSLSGMESTVLLA 120
Oy 121 MAFDRYVAICHLPRHATVTLPRVKIGVAVYRGALMAPLFVROLPPCRSNLHS 180
Db 121 MAFDRYVAICHLPRHATVTLPRVKIGVAVYRGALMAPLFVROLPPCRSNLHS 180
Oy 181 YCLHQDMVNLACDDIRNVYGLIVLISAIGLDSLJSFVLLKTVLGTREADKAF 240
Db 181 YCLHQDMVNLACDDIRNVYGLIVLISAIGLDSLJSFVLLKTVLGTREADKAF 240
Oy 241 GTCVSHVCAVFLFVPPIGLSWHRFSKRDRSPPLPVIANIYLVPPLNPVYGTKE 300
Db 241 GTCVSHVCAVFLFVPPIGLSWHRFSKRDRSPPLPVIANIYLVPPLNPVYGTKE 300
Oy 301 IROIRLRLFHVATHASEP 318
Db 301 IROIRLRLFHVATHASEP 318

RESULT 7
US-09-822-827-920
; Sequence 920, Application US/09822827
; Patent No. US2002016680A1
; GENERAL INFORMATION:
; APPLICANT: ZOPLYA, SERGEY
; APPLICANT: STRYER, LUBERT
; APPLICANT: STRYER, LUBERT
; APPLICANT: STRYER, LUBERT
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 070003-027150
; CURRENT APPLICATION NUMBER: US/09/886, 055
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/213, 812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-886-055-91
Query Match 100.0%; score 1623; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147; Mismatches 0; Indels 0; Gaps 0;
Matches 318; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
Oy 1 MMYDPNGNESSATYFILIGPGLQEEQFWAPLPCSLXLAUGNLTIIYVTERHSHE 60
Db 1 MMYDPNGNESSATYFILIGPGLQEEQFWAPLPCSLXLAUGNLTIIYVTERHSHE 60

QY 61 PHVPLMGSIDILSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 120

Db 61 PHVPLMGSIDILSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 120

QY 121 MAFDRYVAICHPRLRHTAVTLPTRVKTIGVAAVRGALMAPLFVKQLPFCRSNTLHS 180

Db 121 MAFDRYVAICHPRLRHTAVTLPTRVKTIGVAAVRGALMAPLFVKQLPFCRSNTLHS 180

QY 181 YCIRHQDVKLACCDIRYVWGLIVIVISAGIDSLISFSYLKTVGL-TREAAKAF 240

Db 181 YCIRHQDVKLACCDIRYVWGLIVIVISAGIDSLISFSYLKTVGL-TREAAKAF 240

QY 241 GCVVSHVCAVTFVYVPEIGLSMVRFSKRDSPLPVILANTYLVPVPLNPVYGVTK 300

Db 241 GCVVSHVCAVTFVYVPEIGLSMVRFSKRDSPLPVILANTYLVPVPLNPVYGVTK 300

QY 301 IGRQIRLRFHVAHASEP 318

Db 301 IGRQIRLRFHVAHASEP 318

RESULT 9

US-09-968-033C-4

; Sequence 4, Application US/09968033C

; Patent No. US20020168717A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, et al.

; TITLE OF INVENTION: Human Prostate Specific G-Protein Receptor HPRAJ70

; CURRENT APPLICATION NUMBER: US/09/968,033C

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/237,275

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 09/339,115

; PRIOR FILING DATE: 1999-06-24

; PRIOR APPLICATION NUMBER: 09/053,303

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 08/465,980

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-968-033C-4

Query Match 60.6%; Score 983; DB 9; Length 320;

Best Local Similarity 59.8%; Pred. No. 3 2e-86; Mismatches 183; Conservative 54; Indels 2; Gaps 2;

Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESSAYTFLIGLIGLEAFQWFLAPLCSLTLAVGNLTITVYVTEHSLHEPMYIFLC 67

Db 5 NFTHAT-FVLLIGIPGLEKAEHFWGFPLSMYVWAMPGNCIVVFWTRERSLHAPMFLC 63

Db 5 NFTHAT-FVLLIGIPGLEKAEHFWGFPLSMYVWAMPGNCIVVFWTRERSLHAPMFLC 63

QY 68 MUSGIDLISSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 127

Db 68 MUSGIDLISSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 127

Db 64 MUSGIDLISSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 127

QY 188 MRLACDDIRVNVWGLIVIVISAGIDSLISFSYLKTVGL-TREAAKAFGVSH 246

Db 188 MRLACDDIRVNVWGLIVIVISAGIDSLISFSYLKTVGL-TREAAKAFGVSH 246

QY 184 MRLAYADTLPNVYGLTALLVMGVYDVMFISLSYFLIRTLQPLPSKSERAKAFGVSH 243

Db 184 MRLAYADTLPNVYGLTALLVMGVYDVMFISLSYFLIRTLQPLPSKSERAKAFGVSH 243

QY 247 VCAVTFYVPEIGLSMVRFSKRDSPLPVILANTYLVPVPLNPVYGVTKERQRL 306

Db 247 VCAVTFYVPEIGLSMVRFSKRDSPLPVILANTYLVPVPLNPVYGVTKERQRL 306

QY 244 IGVVLAFLYVPLGLSVHFGNSLHPIVRVWMDIVLLPPVNPVNPVYGVTKERQRL 303

Db 244 IGVVLAFLYVPLGLSVHFGNSLHPIVRVWMDIVLLPPVNPVNPVYGVTKERQRL 303

QY 307 RLFHVA 312

Db 307 RLFHVA 312

Db 304 AMPKIS 309

RESULT 10

US-10-012-896-527

; Sequence 527, Application US/10012896

; Publication No. US20020183251A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Ruqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Rettner, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Davy, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Derrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Ajun

; APPLICANT: Skeky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hurlai, John

; APPLICANT: McHeile, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinalis de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; APPLICANT: Watanabe, Toshihiro

; APPLICANT: Meagher, Madeline Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C27

; CURRENT APPLICATION NUMBER: US/10/012,896

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 1011

; SOFTWARE: FastSEQ for Windows Version: 3.0

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-012-896-527

Query Match 60.6%; Score 983; DB 9; Length 320;

Best Local Similarity 59.8%; Pred. No. 3 2e-86; Mismatches 183; Conservative 54; Indels 2; Gaps 2;

Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESSAYTFLIGLIGLEAFQWFLAPLCSLTLAVGNLTITVYVTEHSLHEPMYIFLC 67

Db 5 NFTHAT-FVLLIGIPGLEKAEHFWGFPLSMYVWAMPGNCIVVFWTRERSLHAPMFLC 63

Db 5 NFTHAT-FVLLIGIPGLEKAEHFWGFPLSMYVWAMPGNCIVVFWTRERSLHAPMFLC 63

QY 68 MUSGIDLISSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 127

Db 68 MUSGIDLISSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 127

Db 64 MUSGIDLISSTSSMPKMAIFENNSTIOPDACLQMAFHSLSMESTVLA 127

RESULT 11
 US-09-895-793-527
 ; Sequence 527, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Rettner, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Shekly, Yasir A.W.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Shekly, Yasir A.W.
 ; APPLICANT: Rettner, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Shekly, Yasir A.W.
 ; APPLICANT: Rettner, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Hurl, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C26
 ; CURRENT APPLICATION NUMBER: US/09/895,793
 ; CURRENT FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 990
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 527
 ; LENGTH: 320
 ; ORGANISM: Homo sapiens
 ; US-09-895-793-527
 ;
 Query Match 60.6%; Score 983; DB 9; Length 320;
 Best Local Similarity 59.8%; Pred. No. 3.2e-85;
 Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;
 Query 8 NESSATVFLIGLIGLEEAQWLAFLPCLSLXLYAVIGNLTIVYVTEHSLHEPMYIFC 67
 Db 5 NTHAT-FVLIGIPGLEKAHFWGFFPLMSMTWAMFGNCIVWVIRTERSHAPMYIFLC 63
 Query 68 MLSGIDLISSTSSMPRMLAIWFNSTIOPFACLLQMFAMHLSGMSESTVILAMAFDRYV 127
 Db 64 MLAIDALSTSTMPKILALFWFDSRBSIFEAQTLQMFAMHLSGMSESTVILAMAFDRYV 123
 Query 128 ATCHPLRHATVTLPRVTKIGVAUVRGAALMAPLFVKOLPFCRNSNLSHSYCHQDV 187
 Db 124 ATCHPLRHATVTLPRVTKIGVAUVRGAALMAPLFVKOLPFCRNSNLSHSYCHQDV 183
 Query 188 MKAACDDIRVNVYGLIVISIGLDSLLSISFSYLLTKVGL-TREAAQAKAGTCVSH 246
 Db 184 MKAACDDIRVNVYGLIVISIGLDSLLSISFSYLLTKVGL-TREAAQAKAGTCVSH 243
 Query 247 VCAVFIYVPLIGLSMWHRSKRRDSSPLPVILANTILYLPVLPNLPVLYGKTKERQRL 306
 Db 244 IGVVLAFTPLNVLIGLSVYHREGNSLHPVIRVVMGDIVLILPPVINVPIYGAQKQIKRVL 303
 Query 307 RLEHVA 312
 ;
 Db 304 AMEKIS 309
 ;
 ; RESULT 13
 ; US-09-759-143-527
 ; Sequence 527, Application US/09759143
 ; Patent No. US20020022483A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.

RESULT 12
 US-09-895-814-527
 ; Sequence 527, Application US/09895814
 ;
 ;

APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Rettter, Marc W.
 APPLICANT: Stoik, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel

APPLICANT: Wang, Ajun
 APPLICANT: Skeley, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.421C23
 CURRENT APPLICATION NUMBER: US09/759,143
 CURRENT FILING DATE: 2001-01-12
 NUMBER OF SEQ ID NOS: 934
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 527
 LENGTH: 320
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-09-759-143-527

Query Match 60 6%; Score 983; DB 10; Length 320;
 Best Local Similarity 59 8%; Pred. No. 3.2e-86; Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2; Gaps

QY 8 NESSAVYFTLGLPDLLEQFWMLAPLPCSLXTLAVLGNLITIIVYRTESLHPEYIFLC 67
 Db 5 NFTATH-FVLLIGPGLERKHFVWGFPLLSMVVAMFGNCIVVFTVTERSHADPLFC 63

QY 68 MLSGDILSTSSEMKMLAFWENSTTDFDACLQMLAFHSLSGMESTVLLAMAFDRY 127
 Db 64 MLLAIDLALSSTMPKILLFWEDSREISFEACLTOMFTHALSAESTILLAMAFDRY 123

QY 128 AICHLRHAATLPLRVTKGVAVVRGALMAPLIPVKOLPPCRSNLISHSCLHODV 187
 Db 5 NFTATH-FVLLIGPGLERKHFVWGFPLLSMVVAMFGNCIVVFTVTERSHADPLFC 63

QY 68 MLSGDILSTSSEMKMLAFWENSTTDFDACLQMLAFHSLSGMESTVLLAMAFDRY 127
 Db 124 AICHLRHAATLPLRVTKGVAVVRGALMAPLIPVKOLPPCRSNLISHSCLHODV 183

QY 188 MRLACDDIRNVVGLIVLIVISAIGDLSLPSYLLKWLKG-TREAQAKGTCVSH 246
 Db 184 MRLAYADLPLNVVGLITAILVGMGVDMFTSLSPPLKRLAFCHSNLISHSCLHODV 243

QY 247 VCAVFLFVYVPLIGSMVHRFSKRDSPPLPVTLANTYLVPVLPVLPVIVGVKTKEROTL 305
 Db 244 IGVVLAFLVPLIGLSVVRFGNSLAPIVRVVMGDYLILLPPVNPVNPVYKAKTKIRTVL 303

QY 307 RLPHVA 312
 Db 304 AMFKIS 309

RESULT 14
 US-09-759-143-527
 ; Sequence 527, Application US/09700669
 ; Patent No. US2002005197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangzhen
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Rettter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeley, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; APPLICANT: Hurl, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Hurl, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.

GENERAL INFORMATION:
 ; APPLICANT: Ali, Shuijia
 ; APPLICANT: Cafferkey, Robert
 ; APPLICANT: Recipon, Herve
 ; APPLICANT: Sun, Yonming
 ; TITLE OF INVENTION: Method of diagnosing, monitoring, staging, imaging and
 ; TITLE OF INVENTION: Treating Prostate Cancer
 ; FILE REFERENCE: DEX-0119
 ; CURRENT APPLICATION NUMBER: US/09/759,018
 ; CURRENT FILING DATE: 2000-12-04
 ; CURRENT APPLICATION NUMBER: 60/169,083
 ; PRIORITY FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 320
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-09-730-018-7

Query Match 60 6%; Score 983; DB 10; Length 320;
 Best Local Similarity 59 8%; Pred. No. 3.2e-86; Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2; Gaps

QY 8 NESSAVYFTLGLPDLLEQFWMLAPLPCSLXTLAVLGNLITIIVYRTESLHPEYIFLC 67
 Db 5 NFTATH-FVLLIGPGLERKHFVWGFPLLSMVVAMFGNCIVVFTVTERSHADPLFC 63

QY 68 MLSGDILSTSSEMKMLAFWENSTTDFDACLQMLAFHSLSGMESTVLLAMAFDRY 127
 Db 64 MLLAIDLALSSTMPKILLFWEDSREISFEACLTOMFTHALSAESTILLAMAFDRY 123

QY 128 AICHLRHAATLPLRVTKGVAVVRGALMAPLIPVKOLPPCRSNLISHSCLHODV 187
 Db 124 AICHLRHAATLPLRVTKGVAVVRGALMAPLIPVKOLPPCRSNLISHSCLHODV 183

QY 188 MRLACDDIRNVVGLIVLIVISAIGDLSLPSYLLKWLKG-TREAQAKGTCVSH 246
 Db 184 MRLAYADLPLNVVGLITAILVGMGVDMFTSLSPPLKRLAFCHSNLISHSCLHODV 243

QY 247 VCAVFLFVYVPLIGSMVHRFSKRDSPPLPVTLANTYLVPVLPVLPVIVGVKTKEROTL 305
 Db 244 IGVVLAFLVPLIGLSVVRFGNSLAPIVRVVMGDYLILLPPVNPVNPVYKAKTKIRTVL 303

QY 307 RLPHVA 312
 Db 304 AMFKIS 309

RESULT 15
 US-09-780-669-527
 ; Sequence 527, Application US/09700669
 ; Patent No. US2002005197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangzhen
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Rettter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeley, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; APPLICANT: Hurl, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Hurl, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.

US-09-780-669-527

Query Match 60.6%; Score 983; DB 10; Length 320;
 Best Local Similarity 59.8%; Pred. NO. 3. 2e-86;
 Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

Search completed: March 26, 2003, 10:05:08
Job time : 16 secs

卷之三

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model.

Run on: March 26, 2003, 09:53:07 ; Search time: 46 Seconds

(without alignments) (664.581 Million cell) updates/sec

Title: US-09-966-459a-2

Perfect score: 1623

Sequence: 1 MWVDFENGNESSAYVFLIGH.....KEIRORILRLFHVATHASEP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73;*

1: pix1;*
 2: pix2;*
 3: pix3;*
 4: pix4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	551	33.9	292	2 A60547	hypothetical protein (HPPH breakpoint 3' region) - human (fragment)
2	477.5	29.4	313	2 E45774	odorant receptor 8
3	453	27.9	307	2 S29710	olfactory receptor
4	440	27.1	312	2 A46247	olfactory receptor
5	434.5	26.8	312	2 I23701	olfactory receptor
6	434.5	26.8	319	2 JC524	olfactory receptor
7	433.5	26.7	312	2 S29708	olfactory receptor
8	431.5	26.6	328	2 G45774	odorant receptor 2
9	431.5	26.6	310	2 E23701	olfactory receptor
10	431.5	26.6	314	2 S20572	olfactory receptor
11	425.5	26.2	314	2 A37286	olfactory receptor
12	424.5	26.2	321	2 H45774	odorant receptor 3
13	422.5	26.0	305	2 S29711	olfactory receptor 0
14	420.5	25.9	314	2 S29707	olfactory receptor
15	418.5	25.8	309	1 S51356	olfactory receptor
16	415	25.6	344	2 I45774	odorant receptor 1
17	413	25.4	312	2 A48413	probable olfactory
18	411.5	25.4	311	2 JC5200	chemoreceptor TB33
19	411	25.3	160	2 S58066	probable olfactory
20	406.5	25.0	313	2 S20571	olfactory receptor
21	406.5	24.9	311	2 C23701	olfactory receptor
22	405	24.9	317	2 F45774	odorant receptor 4
23	404.5	24.9	313	2 B23701	olfactory receptor
24	401.5	24.7	312	2 G23701	olfactory receptor
25	399.5	24.6	312	2 H23701	olfactory receptor
26	399.5	24.6	318	2 A45774	odorant receptor 3
27	399.5	24.6	328	2 D45774	odorant receptor 3
28	395.5	24.5	328	2 B45774	odorant receptor 3
29	394.5	24.3	320	2 S20573	olfactory receptor

ALIGNMENTS

RESULT 1
 A60547
 hypothetical protein (HPPH breakpoint 3' region) - human (fragment)

N;Alternate names: olfactory receptor homolog
 C;Species: Homo sapiens (man)

C;Accession: 17-Aug-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999

R;Reingold, E.A.; Forget, B.G.

Blood 74, 2178-2186, 1989

A;Title: The breakpoint of a large deletion causing hereditary persistence of fetal

A;Reference number: A60547; MUID:90028751; PMID:2478223

A;Molecule type: DNA
 A;Residues: 1-292 <FEI>

C;Superfamily: olfactory receptor OR14

Query Match 33.9%; Score 551; DB 2; Length 292;
 Best Local Similarity 41.0%; Pred. No. 1.8e-41; Matches 114; Conservative 50; Mismatches 92; Indels 22; Gaps 6;

Db 29 LIGLGLPGLEEAQMLAFLPCLSLVLYLAVIGNLTIVYIVRTEHSIHEPMYIFLCMLSGIDILL 76

Qy 17 LIGLGLPGLEEAQMLAFLPCLSLVLYLAVIGNLTIVYIVRTEHSIHEPMYIFLCMLSGIDILL 76

Db 29 LIGLGLPGLEEAQMLAFLPCLSLVLYLAVIGNLTIVYIVRTEHSIHEPMYIFLCMLSGIDILL 76

Qy 77 STSSMPKMLAIFWNS-TTIQDACLQKMAFH-SLSGMMESTVLLAMAFDRYVIAICPLR 134

Db 89 ASSIMPKMGYSGMLCKLSILPAC--FNVYVPHPIAGIESGILVANALDRYVIAICPLR 145

Qy 135 HAVTLVLPRTKIGVAWRGALMAPLPVFK-QLPFCRSNMLSHSYCLRHODVMLKACD 193

Db 146 HANIFTHOLWVQIQTGMVTLRAILVLPCHVLLIKRCFQFVHTWVSHSYCERHAIKLA 205

Qy 194 DIRVNVVYGLIVITISAIGDLSLISFSTLILKTVGL-TREQAQAFGTCVSHVCAFI 252

Db 206 IIVVNVKIGLFWVAFPTVAGFDLWITLISIQITVFRIPQOKERAFKAPNCTIAHICVFLQ 265

Qy 253 FVPPFGLISVWRFKRSRDPSPVILAMVILVNPVNL 290

Db 266 FVLLAFFSFPTHRFGSH-----IPPYIH 288

RESULT 2
 E45774
 odorant receptor 8 - channel catfish
 C;Species: Ictalurus punctatus (channel catfish)
 C;Date: 20-Feb-1995 #sequence_change 26-Aug-1999
 C;Accession: E45774
 R;Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
 Cell 72, 657-666, 1993
 A;Title: The family of genes encoding odorant receptors in the channel catfish.
 A;Reference number: E45774; MUID:93201590; PMID:7916654

A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-513 <RGA>
 A; Experimental source: olfactory epithelium
 A; Note: sequence extracted from NCBI backbone (NCBIP:127748)
 C; Superfamily: olfactory receptor OR14
 C; Keywords: olfaction; transmembrane protein

Query Match 29.4%; Score 477.5; DB 2; Length 313;
 Best Local Similarity 34.4%; Pred. No. 6.7e-35;
 Matches 106; Conservative 65; Mismatches 132; Indels 5; Gaps 4;
 QY 2 RVDPPNNESSATYFILGPGLEEAQFWPLASVLYAVGLGMLIIVRTERSLHEP 61
 Db 1 MLAPQONISPTT-FILTGFIDIGEWGAPLSPISPIVLMPLSSTSNLILISORALHSP 59
 QY 62 MYFLFLMGSIDILISTSSHPKMLAIFWENSTTIDFACDILQMAIHSLSGMESTVLLAM 121
 Db 60 MCILQGLMVAWDSLAPIFCIPNMLISPLFWKGTSILVGCIVOMPCICAGTFQSTILLW 119
 Db 122 AFDRTVTAICHLPLRHATVTLPRVTKIGAVAVVRGALMAPLPVFKOLPFCRSNLSLHSY 181
 Db 120 ALDRFAICRPLYKQYGMGMNPLKPIFPPVIRNFITIVSHAGKLPTCEHIDCV 179

QY 182 CLHQMLAKLACDDIRNIVVGLIVISAIGLSDLISFYLLIKVLTREQAARG 241
 Db 180 CERHMLVOLACGGSINNAAGLIVLTFIADFTITSYTIVIVSIL-RSGKACLKAVN 238
 QY 242 TCVSHVCAVFTYVPPFPIGLSMVHRSKRRDPLP-VILANIYLVPPVLPVIVGVKTE 300
 Db 239 TCITHIIVMVSITPLAIIATSYR--RNPSPSSEVLSMPLTIPSCENPIVGVKTE 295

QY 301 IQRQIRL 308
 Db 297 IREQFLKL 304

RESULT 3
 S29710
 olfactory receptor OR18 - rat
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C; Accession: S29710
 R; Raming, R.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breen, Nature 361, 353-356, 1993
 A; Title: Cloning and expression of odorant receptors.
 A; Reference number: S29707; MUID:93149273; PMID:7678922
 A; Accession: S29710
 A; Molecule type: mRNA
 A; Residues: 1-307 <RGA>
 C; Superfamily: olfactory receptor OR14

Query Match 27.9%; Score 453; DB 2; Length 307;
 Best Local Similarity 33.6%; Pred. No. 9.8e-33;
 Matches 107; Conservative 64; Mismatches 125; Indels 22; Gaps 7;

RESULT 4
 A46247
 olfactory receptor OR3 - mouse
 C; Species: Mus musculus (house mouse)
 C; Accession: A46247
 R; Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinen, Proc. Natl. Acad. Sci. U.S.A. 89, 8848-8852, 1992
 A; Title: Spatial pattern of receptor expression in the olfactory epithelium.
 A; Reference number: A46247; MUID:9328384; PMID:1394038
 A; Accession: A46247
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: nucleic acid
 A; Residues: 1-312 <RGA>
 A; Cross-references: GB:m84005; NID:9200153; PID:AAA39862.1; PID:9200154
 A; Note: sequence extracted from NCBI backbone (NCBIP:115362)
 C; Superfamily: olfactory receptor OR14

Query Match 27.1%; Score 440; DB 2; Length 312;
 Best Local Similarity 34.6%; Pred. No. 1.4e-31;
 Matches 113; Conservative 65; Mismatches 123; Indels 26; Gaps 11;

QY 1 RVDPPNNESSATYFILG--PGLEAFWALAPLICSLXIAVGLNLTIVYTERHS 57
 Db 1 MEVDSDN--SSSGTFTIMGSDPHPHETIFFAV--ILASITYLTGVNLTTLSRUDAR 54
 QY 58 LHEPMTFLCMMSIDILISTSSHPKMLAIFWENSTTIDFACDILQMAIHSLSGMESTV 117
 Db 55 LHTPMEFELLSNLSLDAFTSSPVOMLKNWGPDTLISGCTWPLDLYVWLGAFCL 114
 QY 118 LLLAMADRYVATICHPLRHATVTLPRVTKIGAV--VRGAALMAPLPVFKOLPFCRSN 175
 Db 115 LVVMAFDRVAVCRPLHMTVAN-PRLC-WGLAISWNLGGLNSVIOSTFTLQLPCCGR 172
 QY 176 ILSHSTCLHQDWMKLAACDDIRN--VYGLIVIISAIGLSDLISFYLLIKTVGL-T 232
 Db 173 KYDNFLCEVPMAPKILACGGSINNAEAVNGVCTFTTVPVSVTIV-SYCFRQAVKIRS 230
 QY 233 REAQAKAFTCVSHVCAVFTYVPPFPIGLSMVHRSKRRDPLP-VILANIYLVPPVLPVIL 289
 Db 231 VEGRRAKFTCVSHVCAVFTYVPPFPIGLSMVHRSKRRDPLP-VILANIYLVPPVLPVIL 285
 QY 290 NPIVGVKTEKTRQIRLRFHVATHAS 316
 Db 286 NPLIYTNRKEVKGALGLGKGGRAS 312

RESULT 5
 I23701
 olfactory receptor OR4 - rat
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C; Accession: I23701
 R; Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A; Title: A novel multigene family may encode odorant receptors: a molecular basis for
 A; Reference number: A23701; MUID:9191556; PMID:1840504
 A; Accession: I23701
 A; Status: nucleic acid sequence not shown

A; Molecule type: mRNA
 A; Residues: 1-312 <RGA>
 A; Cross-references: GB:W64391; NID:9205843; PID:AAA41754.1; PID:9205844
 C; Superfamily: olfactory receptor OR14
 C; Keywords: G protein-coupled receptor; transmembrane protein

QY 184 HQDVKLACDDIRNVVYGLIVI---ISAGLDSLISSYLLIKTVGLTREQAAKA 239
 Db 179 MSLPLVLAETD--"YFIGLTVIANGVNCIVTIFVLL-SYGTILRSIKTOSGRRKA 234
 QY 240 FGTCVSHVCAVFTYVPP--FGLSMVHRSKRRDPLPVLVANILVPPVLPVITVYGVK 297

Query Match 26.8%; Score 434.5; DB 2; Length 312;
 Best Local Similarity 33.5%; Pred. No. 4.4e-31; Mismatches 105; Conservative 64; Indels 25; Gaps 7; Matches 105; Conserveative 64; Mismatches 119; Indels 25; Gaps 7;

QY 8 NESSATYFLIGGLEAQFWLAFPLSLYLVAVGNNTIVYVTERHSLHEPMYTC 67
 Db 5 NOTVLSIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 64
 QY 68 MUSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 67
 Db 65 NLSRFSDFCSYSSVMPKMLQNMOSQPSISYTGCLQLYFEMVQDMESFLVVMAYDRV 124
 QY 128 ALKPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 181
 Db 125 AICPPLRTTMS---TKFCASLVLWMLMLTALHTL-LIARISFCERNVILFF 178
 QY 182 CLFDQMLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREA 235
 Db 179 CDTSLALKLSCSDIVNEMLITLGLLIII----PFLLIVSIVRIFPSKPSQD 233
 QY 236 QAKAFGTYSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYG 295
 Db 234 IYKVFSTCGSHLSVWVLTGTYGIGYLCP--SANNSTVKEIAMMMYTWTPLNPNPIYS 291
 QY 296 VTKKEIRQLRL 308
 Db 292 LRRNDMKKALIRV 304

RESULT 6

JC5624 olfactory receptor HTRCR92 - human
 C;Species: Homo sapiens (man)
 C;Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000
 C;Accession: JC5624; S58003
 R.Vanderhaeghen, P.; Schurmanns, S.; Vassart, G.; Parmentier, M.
 Biochem. Biophys. Res. Commun. 237, 283-287, 1997
 A;Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed in olfactory receptor HTRCR92 - human
 A;Reference number: JC5624; MUID:97415789; PMID:9268701
 A;Contents: Testis
 A;Accession: JC5624
 A;Molecule type: mRNA
 A;Residues: J-319 <WAN>
 A;Cross references: GB:X10530; NID:92792017; PID:CAA71558.1; PID:92792018
 R.Vanderhaeghen, P.; Schurmanns, S.; Vassart, G.; Parmentier, M.
 submitted to the EMBL Data Library, July 1995
 A;Description: Male germ cells from several mammalian species express a specific repertoire of olfactory receptor genes
 A;Reference number: S57995
 A;Accession: S58003
 A;Molecule type: mRNA
 A;Residues: 126-282 <WAN>
 A;Cross references: EMBL:X09677; NID:9902337; PID:CAA61824.1; PID:9902338
 C;Genetics:
 C;Map position: 19p13.1
 C;Function:
 A;Description: involved in control of sperm physiology
 C;Superfamily: olfactory receptor OR14
 C;Keywords: G protein-coupled receptor; transmembrane protein
 F;26-48/Domain: transmembrane #status predicted <TM>
 F;58-79/Domain: transmembrane #status predicted <TM>
 F;101-120/Domain: transmembrane #status predicted <TM>
 F;140-164/Domain: transmembrane #status predicted <TM>
 F;197-218/Domain: transmembrane #status predicted <TM>
 F;260-281/Domain: transmembrane #status predicted <TM>
 F;272-292/Domain: transmembrane #status predicted <TM>
 Query Match 26.8%; Score 434.5; DB 2; Length 319;
 Best Local Similarity 33.7%; Pred. No. 4.5e-31;
 Matches 103; Conservative 70; Mismatches 118; Indels 15; Gaps 8;

QY 7 GNRESSATYFLIGLIG--PGLEEAQFWLAFPLSLYLVAVGNNTIVYVTERHSLHEPMYTC 63
 Db 4 GNDQIISFLIGQSFQGLQPLFGL--FLMSLIVVIGLMLIATISSHLHTMY 60

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

RESULT 7

S29708 olfactory receptor OR12 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C;Accession: S29708
 R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.;
 Nature 361, 353-356, 1993
 A;Title: Cloning and expression of odorant receptors
 A;Reference number: S29707; MUID:93149273; PMID:678922
 A;Molecule type: mRNA
 A;Residues: 1-312 <RAN>
 C;Superfamily: olfactory receptor OR14

Query Match 26.7%; Score 433.5; DB 2; Length 312;
 Best Local Similarity 32.0%; Pred. No. 5.4e-31; Mismatches 99; Conservative 74; Indels 17; Gaps 6; Matches 99; Conserveative 74; Mismatches 119; Indels 17; Gaps 6;

QY 8 NESSATYFLIGGLEAQFWLAFPLSLYLVAVGNNTIVYVTERHSLHEPMYTC 65
 Db 5 NOTVLSIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 62
 QY 66 LCMLSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 125
 Db 63 LSNLNSFSDLSFSSVMPKMLQNMONDTSITVYTGCLQYFMSWFMFAGHEIFLVMAYDR 122
 QY 126 YVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 185
 Db 123 YVACIPLRHTSISMPKFCVCLGSLSWFLVLSLHLIARISFCERNVIFHFCDS 182
 QY 185 DVMKLAACDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 183 ALKKLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 308
 Db 295 DIKEALVR 304

RESULT 8

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
 Db 180 ELNQVIQLACSDSFLNHNWVYFTVALLGGPLTGIL-PSYKLISSHAISSQKKA 237
 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
 Db 238 FSTCASHLSVSLFYGAILGVYL-SSAATRNSHSSATASVSMVVVTPLNPNPIYSLRK 295
 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

QY 64 IFICLMSGIDILLISTSSMPKMLAIFWNSTIQFACILQMLAHSLSMESTVILAMAFR 123
 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
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 Db 296 DIKRAL 301

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 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
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 QY 240 FGTCVSHVCAVEIIFTVPEIGLSMWHRSKRRDPLPVLTANITYLVPPLNPIYGK 299
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 QY 300 EIRQRI 305
 Db 296 DIKRAL 301

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 Db 61 FFILSNLSFADICVISTTIPKMLNQIOTQNKVITVIACLQMYFILFAGFENELLSVNA 120
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 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
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 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
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 QY 124 DRYVATCPLRRAVTLPLRTRKIGAVW----RGALMAPLPIKOLPFCRNLISY 182
 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY 183 LHQDVKLACDDDIRVN----VYVGLIVIISAGLSDLSLISYLLIKTVGL-TREAQKA 239
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 Db 296 DIKRAL 301

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 Db 121 DRFVATCPLR-HYVYTMNPHCGLLVLASLTSMSALTSQILMVRISCTALETPHFC 179
 QY

A; Status:	nucleic acid sequence not shown; not compared with conceptual transl
A; Molecule type:	mRNA
A; Residues:	193-236 <BUC>
A; Cross-references:	GB: M64375; NID: 920811; PIDN: AAA41738.1; PID: 9205812
C; Superfamily:	olfactory receptor OR14
C; Keywords:	G protein-coupled receptor; membrane protein
Query Match	25.9%; Score 420.5; DB 2; Length 314;
Best Local Similarity	31.1%; Pred. No. 7.8e-30;
Matches	103; Conservative 65; Mismatches 119; Indels 15; Gaps 7
Qy	8 NESSAVTFLIGLGLEEQ-FWLAFLPCSLVLYLAVLGNLTIVVRTENSLHEPTIF 65
Db	5 NOTVISOITLGLGIPPEHOHVAFP-LSMYLITLGMNLLITLDSHLTHPTLF 62
Qy	66 LCMGSDIDTLISTSSMPKMLAIFWNSTTIFDACLQMFIAHSLSGMESTVLLAMAFDR 125
Db	63 LSLMFSFSDLCFSSTVMPKLLQNMOSQVSPSIPYAGLSQLVFFLFFGDLGNELVAMAFDR 122
Qy	126 YVAAVCHPLRHAVTILPRTKIGYAAVWRQALM--APL-PVFIKOLPFCRSNLSHSHY 181
Db	123 YVAAVCFPLHYSINS---PKLCVSLVLSWVLSWLTTEHAMLTILMARNLSFCEDNVIPHFF 178
Qy	182 CLQDVMKLAACDIDRNVVYGLVIVISAIGLDSLJLISFVSLVLLKVGTL-TREAQAKF 240
Db	179 CDMSALLKKAICSDTRVNEVTFIVSLSFLVLPFALLTMSVIVRIVSSILKVSSQYKAF 238
Qy	241 GTCVSHVCAVFLVVFPIGSLSMVHRFSKRRDSPLPVILLANLYLLVPWLPNLNPVYKVF 300
Db	239 SSGCASHLSTVSLFVGTIVLICP--SSNNTVKEVMSLMLTVPMLNPPIYSLRNND 296
Qy	301 IR 302
Db	297 IK 298
RESULT 15	
S51356	
olfactory receptor - rat	
C; Species:	Rattus norvegicus (Norway rat)
C; Date:	10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession:	S51356; S47014
R; Gat, U.; Nebraska, E.; Lancet, D.; Natochin, M.	
Eur. J. Biochem. 225, 1157-1168, 1994	
A; Title:	Olfactory receptor proteins. Expression, characterization and partial
A; Reference number:	S47014
A; Accession:	S51356; MUID: 95045546; PMID: 7957207
A; Status:	preliminary
A; Molecule type:	mRNA
A; Residues:	1-309 <GAT>
A; Cross-references:	EMBL: X80671; NID: 9517365; PIDN: CAA56697.1; PID: 9517366
R; Gat, U.; Nebraska, E.; Lancet, D.; Natochin, M.	
submitted to the EMBL Data Library, July 1994	
A; Description:	Olfactory receptor proteins: expression, characterization and partial
A; Reference number:	S47014
A; Accession:	S47014
A; Status:	preliminary
A; Molecule type:	mRNA
A; Residues:	1-309 <GAT>
A; Cross-references:	EMBL: X80671; NID: 9517365; PIDN: CAA56697.1; PID: 9517366
C; Superfamily:	olfactory receptor OR14
Query Match	25.8%; Score 418.5; DB 1; Length 309;
Best Local Similarity	33.0%; Pred. No. 1.1e-29;
Matches	104; Conservative 63; Mismatches 119; Indels 29; Gaps 8
Qy	7 GNESSAVTFLIGLGLEEQ-FWLAFLPCSLVLYLAVLGNLTIVVRTENSLHEPTIFL 66
Db	5 GNHSAAVWVFLVGLTRQPELILPLFLLFLVIVLTVGNGMILLIVSPLRTPMYFL 64
Qy	67 CMLSGDIDLISSTSSPKMLAIFWNSTTIFQDACLQMFIAHSLSGMESTVLLAMAFDR 126
Db	65 SSSPFDYDLYKSTVTPKMLNLFNGKNEITVSECMQFFEFIFWVTEGGLYIATMADFY 124

Search completed: March 26, 2003, 09:57:05
Job time : 48 secs

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OM protein - protein search, using sw model.

Run on:

March 26, 2003, 09:48:21; Search time 25 Seconds

(without alignments) (25.779 Million cell updates/sec

Perfect score: 1623 US-09-966-459a-2

Sequence: 1 MMVDPNGNESSATYFILGL.....KEIRQRILRLFHVATHASEP 318

scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40.0*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	983	60.5	320	1 OXE2_HUMAN	091255 homo sapien
2	981	60.4	320	1 OXE2_RAT	080628 rattus norv
3	872	53.4	312	1 OX2_HUMAN	091343 homo sapien
4	810.5	49.9	314	1 OXIL_HUMAN	091346 homo sapien
5	790.5	49.1	318	1 OYDI_HUMAN	091341 homo sapien
6	778	48.0	315	1 OXML_HUMAN	096rd2 homo sapien
7	763	47.0	317	1 OYB2_HUMAN	090k12 homo sapien
8	755	46.5	312	1 OYAL_HUMAN	095p1 homo sapien
9	728.5	44.9	312	1 OXB2_HUMAN	096rd3 homo sapien
10	708	43.6	313	1 OYEG_HUMAN	09y5p0 homo sapien
11	633	39.0	310	1 OXK4_HUMAN	Q9nq1 homo sapien
12	28.8	319	1 O2S2_HUMAN	P23275 mus musculus	
13	440	27.1	312	1 O115_MOUSE	095221 homo sapien
14	435.5	26.8	314	1 O5T1_HUMAN	P23273 rattus norv
15	434.5	26.8	312	1 OLF4_RAT	015622 homo sapien
16	432.5	26.8	319	1 O7A5_HUMAN	095371 homo sapien
17	431.5	26.6	312	1 O2C1_HUMAN	P23269 rattus norv
18	431.5	26.6	310	1 OLF0_RAT	P20953 homo sapien
19	431.5	26.6	314	1 O1E1_HUMAN	P27887 homo sapien
20	431	26.6	323	1 O1E2_HUMAN	090403 homo sapien
21	430	26.5	311	1 OAH2_HUMAN	095017 homo sapien
22	428.5	26.4	311	1 O6BL_HUMAN	Q95156 canis famili
23	428	26.4	317	1 OLE3_CANEA	Q93749 homo sapien
24	427.5	26.3	312	1 O1FL_HUMAN	Q99zk7 homo sapien
25	426.5	26.3	315	1 OBA1_HUMAN	P22274 rattus norv
26	425.5	26.2	314	1 OLF1_RAT	Q9h207 homo sapien
27	425	26.2	317	1 OAAB_HUMAN	Q9ugf6 homo sapien
28	423.5	26.1	321	1 O5V1_HUMAN	Q96099 homo sapien
29	422.5	26.0	320	1 O7C1_HUMAN	Q13607 homo sapien
30	421	25.9	317	1 O2FL_HUMAN	P77072 gallus gallus
31	420.5	25.9	312	1 OLE6_CHICK	Q15619 homo sapien
32	420.5	25.9	313	1 OICL_HUMAN	P8181 homo sapien
33	420.5	25.9	314	1 OAAB_HUMAN	P8181 homo sapien

ALIGNMENTS

RESULT 1	OXE2_HUMAN	STANDARD:	PRT:	320 AA.
ID	OXE2_HUMAN			
AC	091255;			
DT	16-OCT-2001 (Rel. 40, created)			
DT	16-OCT-2001 (Rel. 40, last sequence update)			
DT	15-JUN-2002 (Rel. 41, last annotation update)			
DE	Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor) (HPRAJ).			
DE	OR2E2 OR PSGR.			
GN				
RA	Xu L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugam N., Sekerhahn I.A., Zou Z., Srikant V., Augustus M., Koschke V., Carter K., McLeod D.G., Moul J.W., Soppet D., Srivastava S.,			
RA	[1]			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE-21002538; PubMed-11118034;			
RA	Xu L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugam N., Sekerhahn I.A., Zou Z., Srikant V., Augustus M., Koschke V., Carter K., McLeod D.G., Moul J.W., Soppet D., Srivastava S.,			
RA	[2]			
RA	SEQUENCE FROM N.A.			
RA	Xia C., Ma W., Liu M.:			
RA	RT "Identification of a prostate-specific G-protein coupled receptor (PSGR) that interacts with G alpha subunit in yeast two hybrid assay." Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RA	[3]			
RA	SEQUENCE FROM N.A.			
RA	RT MEDLINE-2156169; PubMed-11707321;			
RA	Yuan T.T., Toy P., McCrary J.A., Lin R.J., Miyamoto N.G., Kretschmer P.J.;			
RA	RT "Cloning and genetic characterization of an evolutionarily conserved human olfactory receptor that is differentially expressed across species."			
RA	RT Gene 278:41-51(2001).			
RA	[4]			
RA	SEQUENCE FROM N.A.			
RA	RT TISSUE=Prostate;			
RA	RA Strausberg R.;			
RA	RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
RA	RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
CC	-1 - FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1 - SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1 - TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN THE PROSTATE.			
CC	-1 - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).			

Db	304	AMPKIS	309
Qy	128	AICHLERHATVTLTLETRVTKIGVAVNRGALMAPFVKOLPCRSNLSHSYLHQDV	187
Db	125	AICDPLRYATVLTTEVIAAAGGAAARSFITLPLPFLKRLPICSNSVLSHYSYLHPDM	184
Qy	188	MKLACDDDIRNVVIGLIVISAIGGDSLLTSFSYVILKTVIG-LTREQAKAFCGTCVSH	246
Db	185	MRLACADISINSVGLFLVSYTSGDLEFLTSVILSRSWATTSREELKALWCVSH	244
Qy	247	VCAYTFVYVPIGIGSVNHRSSKRROSPVLTANTYLVLPVNLIVYGVTKERTRIL	306
Db	245	ILAVIAYVPMIGVSVHRRGKHVPCVYIHLMSNTLFVPPVNLIVYSAKTRKEERRAIF	304
Qy	307	RLFH 310	
Db	305	RMFH 308	
Qy	1::1		
RP	SEQUENCE FROM N.A.		
RA	Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,		
RA	Felsenfeld G., Groudine M., Hardison R.,		
RP	*Comparative structural and functional analysis of the olfactory		
RT	receptor genes flanking the human and mouse beta-globin gene		
RT	clusters.;		
RL	Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565 (2000).		
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CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
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CC	EMBL: AF137396; AAG41678.1; -.		
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DR	Pfam: PF00001; 7tm_1.		
DR	PRINTS: PRO0237; GPCRHHODPSN.		
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
DR	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
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CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
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CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
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CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
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CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
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CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
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CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		
CC	InterPro: IPR00276; GPCR_Rhodopsn.		
CC	Pfam: PF00001; 7tm_1.		
CC	PRINTS: PRO0237; GPCRHHODPSN.		
CC	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.		
CC	PROSITE: PS00262; G-PROTEIN_RECEP_FL2_1; 1.		
CC	-----		
CC	EMBL: AF137396; AAG41679.1; -.		

RT clusters";
 RL PROG: *Natl. Acad. Sci. U.S.A.* 97:14560-14565(2000).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AR137396; AA41681.1; ALT INIT.
 DR InterPro: IPR00226; GPCR_Rhodpsn.
 DR Pfam: PF0001; 7TM_1; 1.
 DR PRIMIS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE: PS50262; G PROTEIN RECEPTOR_F1_2; 1.
 KW G-Protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 27 50 1 (POTENTIAL).
 FT DOMAIN 51 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 80 2 (POTENTIAL).
 FT DOMAIN 81 101 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 102 121 3 (POTENTIAL).
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 159 4 (POTENTIAL).
 FT DOMAIN 160 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 197 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 260 6 (POTENTIAL).
 FT DOMAIN 261 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 295 7 (POTENTIAL).
 FT DOMAIN 296 315 CYTOPLASMIC (POTENTIAL).
 FT DISLEID 98 190 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 315 AA; 35462 MW; DC19D2P456D2005 CRC64;

Query Match 48.0%; Score 778.5; DB 1; Length 315;
 Best Local Similarity 47.8%; Pred. No. 4.e-52; Mismatches 89; Indels 1; Gaps 1;
 Matches 141; Conservative 64; Mismatches 89; Indels 1; Gaps 1;

QY 15 FILIGLPGLEEAQFLAFLPCSYLIVLAVIGNLTIVYRTERHSIHEPMYIFLQMLSGID 74
 DR 13 FYLTSFPGLEGKHWIFPFMFMVMAISGNCFLILIKTRNPRHTPMYLISLALD 72

QY 75 LISSSMPMLAIFPNSTIQDACLQMFHSLSGESTVLLAMAFDRYVAICHLR 134
 DR 73 GLCVALSTLPTMGFLPNFNSOYHGAQCOLMCFHFSMESSTLIMSFDRFVACHLR 132

QY 135 HAVTIVLPLRPTKGIVAAVRGAALMAPLFVFLQKQLPFRNSNITSHSYCLHQDMKLA 194
 DR 133 YSVITGQDQVVRAGLIVIFRGPATIPFLVLLKAFPGYGSVWHSFCLHQEVIQAC 192

QY 15 FILIGLPGLEEAQFLAFLPCSYLIVLAVIGNLTIVYRTERHSIHEPMYIFLQMLSGID 74
 DR 14 FYLTSFPGLEGKHWIFPFMFMVMAISGNCFLILIKTRNPRHTPMYLISLALD 73

QY 75 LISSSMPMLAIFPNSTIQDACLQMFHSLSGESTVLLAMAFDRYVAICHLR 134
 DR 132 YSVITGQDQVVRAGLIVIFRGPATIPFLVLLKAFPGYGSVWHSFCLHQEVIQAC 192

QY 135 HAVTIVLPLRPTKGIVAAVRGAALMAPLFVFLQKQLPFRNSNITSHSYCLHQDMKLA 194
 DR 134 YTVLWVGPVGRALAVIERSFCIFPVFLKLPFCITNIVHPSYCHIGVARLAC 193

QY 195 IRVNVYGLIVITIAIGLSLILTSYLLIKVYGL-TREADAKAFGCVSHVCAVFLP 253
 DR 194 ITVNWVGSVPTPAVFLDVLVIAVSYLILRAVFLPESQDARHALSTCGSHLCLVLMF 253

QY 254 YVPPIGLSMVRERSKRSPPLPVILANILVLPVLPNPIVYGYKTEIRQRIL-RFLVFA 312
 DR 253 FVPMGLSLVHFRGKXHAPPALHMLANVYLPVPMNPLIYVSKTKEIHLAIKL 307

RESULT 7
 OYB2_HUMAN STANDARD: PRT: 317 AA.
 ID OYB2_HUMAN STANDARD: PRT: 317 AA.
 AC 096RD2;
 DT 15-JUN-2002 (Rel. 41, created)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Olfactory receptor 52B2.
 RN OR5B2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RN SEQUENCE OF 70-287 FROM N.A.
 RA Fuchs T., Malcová B., Linhart C., Sharpen R., Khan M., Herwig R.,
 RA Shamlevich D., Elkow R., Steinbach M., O'Brien J.K., Radefeld U.,
 RA Lehner H., Oelender Z., Gluesman G., Lancet D., Shamir R.;
 RT "DEROG: a practical scheme for deciphering families of genes.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AF399505; AAK94990.1;
 DR InterPro: IPR00226; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE: PS50262; G PROTEIN RECEPTOR_F1_2; 1.
 KW G-Protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 51 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 52 59 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 60 81 2 (POTENTIAL).
 FT DOMAIN 82 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 122 3 (POTENTIAL).
 FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 160 4 (POTENTIAL).
 FT DOMAIN 161 197 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 198 221 5 (POTENTIAL).
 FT DOMAIN 222 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 261 6 (POTENTIAL).
 FT DOMAIN 252 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 277 296 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 297 317 BY SIMILARITY.
 FT DISLEID 99 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 5 5
 SQ SEQUENCE 317 AA; 35462 MW; DB7DB91F8E21 CRC64;

Query Match 47.0%; Score 763; DB 1; Length 317;
 Best Local Similarity 49.2%; Pred. No. 6.5e-51; Mismatches 94; Indels 2; Gaps 2;
 Matches 148; Conservative 57; Mismatches 94; Indels 2; Gaps 2;

QY 15 FILIGLPGLEEAQFLAFLPCSYLIVLAVIGNLTIVYRTERHSIHEPMYIFLQMLSGID 74
 DR 14 FYLTSFPGLEGKHWIFPFMFMVMAISGNCFLILIKTRNPRHTPMYLISLALD 73

QY 75 LISSSMPMLAIFPNSTIQDACLQMFHSLSGESTVLLAMAFDRYVAICHLR 134
 DR 132 YSVITGQDQVVRAGLIVIFRGPATIPFLVLLKAFPGYGSVWHSFCLHQEVIQAC 192

QY 135 HAVTIVLPLRPTKGIVAAVRGAALMAPLFVFLQKQLPFRNSNITSHSYCLHQDMKLA 194
 DR 134 YTVLWVGPVGRALAVIERSFCIFPVFLKLPFCITNIVHPSYCHIGVARLAC 193

QY 195 IRVNVYGLIVITIAIGLSLILTSYLLIKVYGL-TREADAKAFGCVSHVCAVFLP 253
 DR 194 ITVNWVGSVPTPAVFLDVLVIAVSYLILRAVFLPESQDARHALSTCGSHLCLVLMF 253

QY 254 YVPPIGLSMVRERSKRSPPLPVILANILVLPVLPNPIVYGYKTEIRQRIL-RFLVFA 312
 DR 253 FVPMGLSLVHFRGKXHAPPALHMLANVYLPVPMNPLIYVSKTKEIHLAIKL 307

QV	313	T	313	db	314	T	314
RESULT 8							
OR1_HUMAN				STANDARD;		PR1;	312 AA.
ID	OR1_HUMAN						
AC	Q02122;						
DT	16-OCT-2001 (Rel. 40, Last sequence update)						
DT	16-OCT-2001 (Rel. 40, Last annotation update)						
DE	Olfactory receptor 52A1 (HPRH1OR) (H033_beta4).						
GN	OR52A1.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TAXID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE:99433868; PubMed=10512676;						
RA	Feingold E.A., Penny L.A., Nienhuis A.W., Forget B.G., Forget B.G.,						
RA	Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565 (2000).						
RT	An olfactory receptor gene is located in the extended human beta-globin gene cluster and is expressed in erythroid cells.;						
RT	Globin genes cluster and is expressed in erythroid cells.;						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE:20570519; PubMed=11121057;						
RA	Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,						
RA	Felsenfeld G., Groudine M., Hardison R.,						
RT	Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene clusters.;						
RT	Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565 (2000).						
-I- FUNCTION: PUPATIVE ODORANT RECEPTOR.							
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.							
-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.							
CC	-----						
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RP	SEQUENCE FROM N.A.						
RX	OB2_HUMAN						
ID	OB2_HUMAN						
AC	O9Y5P1; O963D4;						
DT	09Y5P1; O963D4;						
DT	16-OCT-2001 (Rel. 40, Last sequence update)						
DT	16-OCT-2001 (Rel. 40, Last annotation update)						
DE	Olfactory receptor 51B2 (H035_beta3).						
GN	OB51B2.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TAXID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE:9238494; PubMed=10220450;						
RA	Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.,						
RA	Bender M.A., Felsenfeld G., Axel R., Groudine M.,						
RT	Conservation of sequence and structure flanking the mouse and human beta-globin loci: the beta-globin genes are embedded within an array of odorant receptor genes.;						
RT	Proc. Natl. Acad. Sci. U.S.A. 96:5125-5134 (1999).						
RL	[2]						
RP	ERRATUM.						
RA	Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.,						
RA	Bender M.A., Felsenfeld G., Axel R., Groudine M.,						
RA	Proc. Natl. Acad. Sci. U.S.A. 96:8307-8307 (1999).						
RN	[3]						
RP	SEQUENCE OF 66-283 FROM N.A.						
RA	Fuchs T., Malecova B., Linhart C., Sharai R., Khen M., Herwig R.,						
RA	Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radloff U.,						
RA	Lehrach H., Oelander Z., Gluesemann G., Lancet D., Shamir R.,						
RA	"DEFOG": a practical scheme for deciphering families of genes.;						
RT	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.						
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.						
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.						
RP	SEQUENCE OF 66-283 FROM N.A.						
RA	Fuchs T., Malecova B., Linhart C., Sharai R., Khen M., Herwig R.,						
RA	Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radloff U.,						
RA	Lehrach H., Oelander Z., Gluesemann G., Lancet D., Shamir R.,						
RA	"DEFOG": a practical scheme for deciphering families of genes.;						
RT	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.						
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.						
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.						
RP	SEQUENCE OF 66-283 FROM N.A.						
RA	Fuchs T., Malecova B., Linhart C., Sharai R., Khen M., Herwig R.,						
RA	Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radloff U.,						
RA	Lehrach H., Oelander Z., Gluesemann G., Lancet D., Shamir R.,						
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RA	Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radloff U.,						
RA	Lehrach H., Oelander Z., Gluesemann G., Lancet D., Shamir R.,						
RA	"DEFOG": a practical scheme for deciphering families of genes.;						

CC
 DR
 EMBL; AF137396; AAD29425; 2;
 DR
 EMBL; AF399503; ARK94989; 1;
 DR
 InterPro; HGNC:14703; OR51B2;
 DR
 Pfam; PP00001; 7tm_1; 1.
 DR
 PROSITE; PS0237; GPROTRHODPSN;
 DR
 PROSITE; PS5062; GPROTRHODPSN;
 KW
 G-protein coupled receptor; transmembrane; Glycoprotein;
 MultiGene family; Olfaction.
 FT
 DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 24 47 1 (POTENTIAL).
 FT
 DOMAIN 48 55 CYTOPLASMIC (POTENTIAL).
 FT
 TRANSMEM 56 77 2 (POTENTIAL).
 FT
 DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 99 118 3 (POTENTIAL).
 FT
 DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
 FT
 TRANSMEM 138 156 4 (POTENTIAL).
 FT
 DOMAIN 157 193 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 194 217 5 (POTENTIAL).
 FT
 DOMAIN 218 234 CYTOPLASMIC (POTENTIAL).
 FT
 TRANSMEM 235 257 6 (POTENTIAL).
 FT
 DOMAIN 258 266 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 273 292 7 (POTENTIAL).
 FT
 DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).
 FT
 DISULFID 95 187 BY SIMILARITY.
 FT
 CARBOHYD 4 N-LINKED (GLCNAC, -) (POTENTIAL).
 SQ 312 AA; 35513 MW; ODA1160267778EDD CRC64;

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 11 SATYFILIGLPLEERQFWLAPLCSLXLIAVIGNLTIVYRTEHSIHEPMVIFCLMS 70
 DB 6 TAPEPLIGEGLAHWISIPEFVYCLLGGMLYLLKHDHSIHEPMYETJMLA 65

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 71 GIDILISTSSMPRLAFLWFNSTTIDQACLIQMFATHSLSGESTVILAMAFDRYVAIC 130
 DB 66 GIDILVLTITMEPTVGMILWNVHREISSYGCFLQAYFHSLSVESGLSLLAMADFRAIR 125

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 131 HPLRHATVLTIPRVTKGVAAVVRGALMAPFLVFTIKOLPCCRNTISHSYCLHDQMLK 190
 DB 126 NPLRVSASIFTWTRVIAVGVGFLRGFLVPLVLRFLPSICKHVTIACFLHQEMRL 185

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 191 ACDDIRNVVGLIVVISAIGDLSLISFSVLLKVLGGL-TREOAQAKSTCVSHVCA 249
 DB 186 ACADDTRNLPIVLSITLFLSLLTFSVLLKVLGGL-TREOAQAKSTCVSHVCA 245

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 250 VFTIYVPIFGLSMVHRSKRRDPLSPVILANLYLVPVLPVNLIVYGVKTKETRQIRL 308
 DB 246 VLIYFTVWMLTIFYREGKVNPEVHIMSTIVFPLPMLNVIVSIRKQIQYIGIRL 304

RESULT 10
 OYEG_HUMAN STANDARD; PRT; 313 AA.
 ID OYEG_HUMAN STANDARD; PRT; 313 AA.
 AC 096RD; 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Olfactory receptor 52B6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE OF 70-287 FROM N.A.
 RA Fuchs T., Malecova B., Linhart C., Sharpen R., Khan M., Herwig R., Smulovitch D., Eikon R., Steinfath M., O'Brien J.K., Radefof U., Lehrach H., Olander Z., Gluesman G., Dancet D., Shamil R.;
 RA

CC
 DR
 EMBL; AE137396; AAD29425; 2;
 DR
 InterPro; IPK000276; GPCR_Rhodpsn.
 DR
 Pfam; PP00001; 7tm_1; 1.
 DR
 PROSITE; PS0237; GPROTRHODPSN;
 DR
 PROSITE; PS0262; GPROTRHODPSN;
 KW
 G-protein coupled receptor; transmembrane; Glycoprotein;
 MultiGene family; Olfaction.
 FT
 DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 24 47 1 (POTENTIAL).
 FT
 DOMAIN 48 55 CYTOPLASMIC (POTENTIAL).
 FT
 TRANSMEM 56 77 2 (POTENTIAL).
 FT
 DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 99 118 3 (POTENTIAL).
 FT
 DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
 FT
 TRANSMEM 138 156 4 (POTENTIAL).
 FT
 DOMAIN 157 193 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 194 217 5 (POTENTIAL).
 FT
 DOMAIN 218 234 CYTOPLASMIC (POTENTIAL).
 FT
 TRANSMEM 235 257 6 (POTENTIAL).
 FT
 DOMAIN 258 266 EXTRACELLULAR (POTENTIAL).
 FT
 TRANSMEM 273 292 7 (POTENTIAL).
 FT
 DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).
 FT
 DISULFID 95 187 BY SIMILARITY.
 FT
 CARBOHYD 4 N-LINKED (GLCNAC, -) (POTENTIAL).
 SQ 312 AA; 35513 MW; ODA1160267778EDD CRC64;

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 11 SATYFILIGLPLEERQFWLAPLCSLXLIAVIGNLTIVYRTEHSIHEPMVIFCLMS 70
 DB 6 TAPEPLIGEGLAHWISIPEFVYCLLGGMLYLLKHDHSIHEPMYETJMLA 65

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 71 GIDILISTSSMPRLAFLWFNSTTIDQACLIQMFATHSLSGESTVILAMAFDRYVAIC 130
 DB 66 GIDILVLTITMEPTVGMILWNVHREISSYGCFLQAYFHSLSVESGLSLLAMADFRAIR 125

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 131 HPLRHATVLTIPRVTKGVAAVVRGALMAPFLVFTIKOLPCCRNTISHSYCLHDQMLK 190
 DB 126 NPLRVSASIFTWTRVIAVGVGFLRGFLVPLVLRFLPSICKHVTIACFLHQEMRL 185

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 191 ACDDIRNVVGLIVVISAIGDLSLISFSVLLKVLGGL-TREOAQAKSTCVSHVCA 249
 DB 186 ACADDTRNLPIVLSITLFLSLLTFSVLLKVLGGL-TREOAQAKSTCVSHVCA 245

Query Match 44.9%; Score 728.5; DB 1; Length 312; Best Local Similarity 44.1%; Pred. No. 2.6e-48; Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1; CTD
 OY 250 VFTIYVPIFGLSMVHRSKRRDPLSPVILANLYLVPVLPVNLIVYGVKTKETRQIRL 308
 DB 246 VLIYFTVWMLTIFYREGKVNPEVHIMSTIVFPLPMLNVIVSIRKQIQYIGIRL 304

RESULT 11
 OX4_HUMAN STANDARD; PRT; 310 AA.
 ID OX4_HUMAN STANDARD; PRT; 310 AA.
 AC 0955PO; 16-OCT-2001 (Rel. 40, Created)

		Matches	122;	Conservative	72;	Mismatches	105;	Indels	2;	Gaps	2;
DT	16-OCT-2001 (Rel. 40, Last sequence update)	QY	10	SSATVFLIGLIPGLERAQFFLAFPLCLSLVIAVLGNLTIVIVREHSLHEPMIFCME	69						
DT	16-OCT-2001 (Rel. 40, Last annotation update)	Db	5	NSAGPFLLPGFLGSRAYHRSMSFVIVSILFENGTLVILWHDHSLPEMVFLAM	64						
DR	Olfactory receptor 51b4 (HORS5/beta1).	QY	70	SGIDILISTSSMPKMAIFPENSTIOFDACLQMAFHSLSGMSVTLLAFAFDYVAI	129						
GN	OR51b4.	Db	65	ADTDLGMTFTMPTVGLVLLDRETAHAACFTOSF-IHSIAVSGILVLAIFCFIAI	123						
OS	Homo sapiens (Human).	QY	130	CHPLRHATVTLPRYTKIGVAVWGAVALAPLVIKOPFCRENTLSYCLQDVK	189						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Db	124	RPLPRYNCILTNSRVMNIGLGLVMRGFMSTIPLTILSYCLVCPYCGSKALLHFLCHODVK	183						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	QY	190	LACDDIRVNWVGLIVIISAGLDSLISLSSYLLIKTIVGL-TREAQAKAFGCVSHVC	248						
OC	OX	Db	184	LACADITENINYPIQTSIPLVLDALIITISYLLIKTIVGIAQSQEAEASLNTCVHSIS	243						
RA	Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.M.,	QY	249	AVFIYVPPFGLSMWRFSKRDRSPAVLIVIYLUPPVNPVYGVKREIRMLR	308						
RA	Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.M.,	Db	244	CVLVPHITWGLSFIHRFGKHAPHVWPITSYVHFLPPVNPVYISIKRQIQSIRI	303						
RL	Proc. Natl. Acad. Sci. U.S.A. 96:8307-8307(1999).	QY	309	F	309						
RN	[3]										
RP	REVISIONS										
RA	REDBANK: 20570519; PubMed:11121057;										
RA	Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,										
RA	Felsenfeld G., Groudine M., Hardison R.,										
RT	*Comparative structural and functional analysis of the olfactory										
RT	receptor genes flanking the human and mouse beta-globin gene										
RT	clusters".										
RT	-I- FUNCTION: PUTATIVE ODORANT RECEPTOR.										
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.										
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.										
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/										
CC	or send an email to license@isb-sib.ch).										
CC	EMBL: AF137396; AAC39426; 2;										
DR	GeneW: HGNC:14708; OR51BA.										
DR	InterPro: IPR000276; GPCR_Rhodpsn.										
DR	Pfam: PF00001; 7tm_1; 1.										
DR	PRINTS: PR00237; GPCR_RHODPSN.										
DR	PROSITE: PS00217; G-PROTEIN_RECEP_FL1_2; 1.										
DR	PROSITE: PS00202; G PROTEIN_RHODPSN.										
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;										
KW	Multigene family; Olfaction.										
DOMAIN	1										
FT	TRANSMEM	24	1	(POTENTIAL).							
FT	DOMAIN	48	55	CYTOSMATIC (POTENTIAL).							
FT	TRANSMEM	56	77	2 (POTENTIAL).							
FT	DOMAIN	78	98	EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM	99	117	3 (POTENTIAL).							
FT	DOMAIN	118	136	CYTOSMATIC (POTENTIAL).							
FT	TRANSMEM	137	155	4 (POTENTIAL).							
FT	DOMAIN	156	192	EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM	193	216	5 (POTENTIAL).							
FT	DOMAIN	217	233	CYTOSMATIC (POTENTIAL).							
FT	TRANSMEM	234	256	6 (POTENTIAL).							
FT	DOMAIN	257	265	EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM	273	291	7 (POTENTIAL).							
FT	DOMAIN	292	310	CYTOSMATIC (POTENTIAL).							
FT	TRANSMEM	95	186	BY SIMILARITY.							
FT	CARBODY	4	4	N-LINKED (GLCNAC -) (POTENTIAL).							
SQ	SEQUENCE	310 AA;	34926 MW;	BFE58363BA2EED7 CRC64;							
Query	Match		39.0%	Score 633; DB 1; Length 310;							
Best	Local	Similarity	40.3%	Pred. No. 4.2e-41;							

RA Evans G.A.;
 RA "Organization and evolution of olfactory receptor genes on human
 RT chromosome 11";
 RT Genomics 53:56-68(1998).
 [2]

SEQUENCE OP 68-283 FROM N.A.
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khan M., Herwig R.,
 RA Shmulevich D., Elkton R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Lehrach H., Olender Z., Gluecksmann G., Lancet D., Shamir R.;
 RT "DEFOG: a practical scheme for deciphering families of genes";
 CC submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC
 CC -I- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; AF055863; AAC70017.1; -.
 DR GenBank; AF399527; ARX5012.1; -.
 DR GenBank; HGNC; 8343; OR5F1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.
 DR PROSITE; PS50562; G-PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 196 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 259 6 (POTENTIAL).
 FT DOMAIN 250 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 35131 MW; C14A9A35CD7683A3 CRC64;

Query Match 26.8%; Score 435.5; DB 1; Length 314;
 Best Local Similarity 32.7%; Pred. No. 3.6e-26;
 Matches 102; Conservative 58; Mismatches 123; Indels 29; Gaps 6;

RA Evans G.A.;
 RA "Organization and evolution of olfactory receptor genes on human
 RT chromosome 11";
 RT Genomics 53:56-68(1998).
 [2]

SEQUENCE OP 68-283 FROM N.A.
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khan M., Herwig R.,
 RA Shmulevich D., Elkton R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Lehrach H., Olender Z., Gluecksmann G., Lancet D., Shamir R.;
 RT "DEFOG: a practical scheme for deciphering families of genes";
 CC submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC
 CC -I- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; AF399527; ARX5012.1; -.
 DR GenBank; AF399527; ARX5012.1; -.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
 DR PROSITE; PS50562; G-PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 100 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 101 120 3 (POTENTIAL).
 FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 140 158 4 (POTENTIAL).
 FT TRANSMEM 159 195 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 196 219 5 (POTENTIAL).
 FT TRANSMEM 237 259 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 250 272 6 (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 312 AA; 35718 MW; 08F08546994B1680 CRC64;

Query Match 26.8%; Score 434.5; DB 1; Length 312;
 Best Local Similarity 33.5%; Pred. No. 4.2e-26;
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;

RA Evans G.A.;
 RA "Organization and evolution of olfactory receptor genes on human
 RT chromosome 11";
 RT Genomics 53:56-68(1998).
 [2]

SEQUENCE OP 68-283 FROM N.A.
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khan M., Herwig R.,
 RA Shmulevich D., Elkton R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Lehrach H., Olender Z., Gluecksmann G., Lancet D., Shamir R.;
 RT "DEFOG: a practical scheme for deciphering families of genes";
 CC submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC
 CC -I- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL; AF055863; AAC70017.1; -.
 DR GenBank; AF399527; ARX5012.1; -.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
 DR PROSITE; PS50562; G-PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 100 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 101 120 3 (POTENTIAL).
 FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 140 158 4 (POTENTIAL).
 FT TRANSMEM 159 195 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 196 219 5 (POTENTIAL).
 FT TRANSMEM 237 259 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 250 272 6 (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 312 AA; 35718 MW; 08F08546994B1680 CRC64;

Query Match 26.8%; Score 434.5; DB 1; Length 312;
 Best Local Similarity 33.5%; Pred. No. 4.2e-26;
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;

Db 234 RHRASFSCASHITAILFYATCIVYLRPSSYSLNQDK---VASVFTVWIPMLNPLI 289.
 QY 294 YGVTKTBIRQRI 305
 Db 290 YSLRSKEVKRKA 301

RESULT 15
 ID OLFA_RAT
 ID OLFA_RAT
 STANDARD; PRT; 312 AA.
 AC P23273;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DR 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Olfactory receptor-like protein 114.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91191556; PubMed=1840504;
 RA BUCK L.; Axel R.;
 RT A novel multigene family may encode odorant receptors: a molecular
 RT basis for odor recognition.;
 RL Cell 65:175-187(1991).
 CC
 CC -I- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL; AF4391; AAC41754.1; -.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
 DR PROSITE; PS50562; G-PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 100 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 101 120 3 (POTENTIAL).
 FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 140 158 4 (POTENTIAL).
 FT TRANSMEM 159 195 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 196 219 5 (POTENTIAL).
 FT TRANSMEM 237 259 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 250 272 6 (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 312 AA; 35718 MW; 08F08546994B1680 CRC64;

Query Match 26.8%; Score 434.5; DB 1; Length 312;
 Best Local Similarity 33.5%; Pred. No. 4.2e-26;
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;

Db	5	NOTLILEFLGLGLPPIPSEYHFLFYALFLAMVLTITLGNLTLIVLVRDLSHAMPMLFLS	64
QY	68	MUSGIDILISSTSSMPKMLAIEWNSTTIOFACCLLQFAISLSGMESTVLLAMAEDRY	127
Db	65	NLFSDFSLCFSSTSSMPKMLQUNQMSQVSFISIYTQCLTQIFFMVFGDMSFLLVMDRY	124
QY	128	ATCHPLRHATVTLTPRVTKIGVAAV-----RGAALMAPLVEIKLPCRSNLHSY	181
Db	125	ATCFLPLRVTTMS---TKFCASLVLWLMUJMTTHALLHTL--LIARLSFCERNVILHFP	178
QY	182	CLHQDVVKLACDDIRV---WVGLIVLISAIGDLSLISFSYSLILKTVGL-TREA	235
Db	179	CDTSALXLTSCSDIYVNEMLVILGGILII-----PFLITMSYVRFESLKFPSIQD	233
QY	236	QAKAFGTCVSHYCAVFLFVYRFTIGLSKHYRFESKRDRDSSPLPVLTANTILVLPVLPNRTYV	295
Db	234	IVKVSTFCGSHLSVVTLFYGTIFGIVLCP--SGNNSTVKEIAMMAMTVVTPMLNPFIYS	291
QY	296	VKEKEIQRRLR 308	
Db	292	LRNDRMERRALIRV 304	

Search completed: March 26, 2003, 09:53:02
Job time : 26 secs

GenCore version 5.1.4_p5-4578
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On protein - protein search, using sw model

Run on:

March 26, 2003, 09:51:52 ; Search time 87 Seconds

(without alignments) 753.138 Million cell updates/sec

Title:

US-09-966-459a-2

Perfect score:

1 MVDPGNGNESSATYFLIGL.....KEIQRQTRLRLFHVATHASEP 318

Sequence:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

671580 seqs, 20607115 residues

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length:

0

Maximum DB seq length:

200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMU21:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Pred - No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No. Score Query Match length DB ID

Description

RESULT 1

08TCB6

08TCB6

08TCB6;

AC

08TCB6;

DT

01-JUN-2002

(TREMBREL.

01-JUN-2002

(TREMBREL.

21, Last sequence update)

DT

01-JUN-2002

(TREMBREL.

21, Last annotation update)

DE

Hypothetical

35.3 kDa protein.

OS

Homo sapiens (Human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

OC

NCBI_TaxID:9606;

RN

[1]

SPSEQUENCE FROM N.A.

RP

TISSUE-LUNG;

RA

Strausberg R.;

RL

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

DR

EMBL: BC022401; AAH22401.1; -.

KW

Hypothetical protein.

SQ

SPSEQUENCE 317 AA; 35271 MW; BC7293AA7FBCA95C CRC64;

Query Match

99.7%; Score 1618; DB 4; Length 317;

Best Local Similarity

100.0%; Pred. No. 1. 6e-137;

Matches: 317; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Description

08tc06 homo sapien

08vg27 mus musculu

08vgvg mus musculu

08vgv9 mus musculu

08vh05 mus musculu

08vh11 mus musculu

08vh26 mus musculu

08vg23 mus musculu

08vh17 mus musculu

08vg22 mus musculu

08vh01 mus musculu

08vg28 mus musculu

08vh04 mus musculu

08vgw0 mus musculu

09eq97 mus musculu

08vgx9 mus musculu

08vh12 mus musculu

08vh15 mus musculu

08vh07 mus musculu

08vg98 mus musculu

08vg97 mus musculu

08vh16 mus musculu

08vf28 mus musculu

08vh12 mus musculu

08vg95 mus musculu

08vg50 mus musculu

08vg66 mus musculu

08vg55 mus musculu

08vh20 mus musculu

08vh19 mus musculu

08vg53 mus musculu

08vg99 mus musculu

08vh14 mus musculu

ALIGNMENTS

RESULT 2

Q8VGZ7. PRELIMINARY; PRT; 317 AA.

ID Q8VGZ7; DT 01-MAR-2002 (TREMBREL. 20, Created)

AC DT 01-MAR-2002 (TREMBREL. 20, last sequence update)

DT 01-MAR-2002 (TREMBREL. 21, Last annotation update)

DE DE Olfactory receptor MOR18-2 (prostate-specific G protein-coupled receptor Ralc).

DB DE OLFR8.

QY 302 RQRILRLFHVATHASEP 318

301 RQRILRLFHVATHASEP 317

RN [1]

RN OS MUS musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TAXID=10090;

RN RN [1]

RN SEQUENCE FROM N.A.

RA RA Zhang X.; Firestein S.J.;

RT RT "The olfactory receptor gene superfamily of the mouse.";

DT RL Nat. Neurosci. 0:0-0(2002).

DT RN [2]

DT SEQUENCE FROM N.A.

RA RA Adams M.;

RA RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RA RA STRAIN=BALB/C;

RA RX MEDLINE=21564169; PubMed=11707321;

RA Yuan T.T.; Toy P.; McClay J.A.; Lin R.J.; Miyamoto N.G.,

RA RA Kretschmer P.J.;

RA RA "Cloning and genetic characterization of an evolutionarily conserved human olfactory receptor that is differentially expressed across species.";

RA RA Gene 278:41-51(2001).

DR DR EMBL; AY073011; AAJ60674_1; -.

DR DR MGD; MGI:215748; Olfr78.

DR DR InterPro; IPR00276; GPCR_Rhodopsn.

DR DR Pfam; PF00001; 7tm_1; 1.

DR DR PROSITE; PS00237; G_PROTEIN_RECER_FL_1; UNKNOWN_1.

DR DR PROSITE; PS50262; G_PROTEIN_RECER_FL_2; 1.

RW RW Receptor.

SEQUENCE 317 AA; 35463 MW; 5A0E59E229852534 CRC64;

Query Match 93.4%; Score 1516; DB 11; Length 317;

Best Local Similarity 93.7%; Pred. No. 2.3e-128;

Matches 296; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 2 MVDPGNGESSATTFILGLPGLEAAOFMLAEPGSLVLYAVGNLTIVYVTERHSLHEP 61

DB 1 MYFGFNSNESSATTFILGLPGLEEVQMLAFLPLCSLYLIAVGNLTIVYVTERHSLHEP 60

QY 62 MYFLCMLGIDILISSSMPKMAIFENSTI1QFDACILQHAFHSISGMESTVILAM 121

61 MYFLCMLGIDILISSSMPKMAIFENSTI1QFDACILQHAFHSISGMESTVILAM 120

DB 122 AEDRYVATCHPLRHLFVATVILPRTVKIGAVAVRGALMAPLVPVTKOLPFCRSNTLHSYH 181

QY 121 AEDRYVATCHPLRHLFVATVILPRTVKIGAVAVRGALMAPLVPVTKOLPFCRSNTLHSYH 180

DB 122 AEDRYVATCHPLRHLFVATVILPRTVKIGAVAVRGALMAPLVPVTKOLPFCRSNTLHSYH 180

QY 182 CLRDQVMLACDPRIVNVTGGLVIVISAGLDSLISFSYLLIKTVGLTREQAKEF 241

DB 181 CLRDQVMLACDPRIVNVTGGLVIVISAGLDSLISFSYLLIKTVGLTREQAKEF 240

QY 242 TCVSHVCAVIFVPPFGLSMWHRFSRDRSPFLPVILANILVLPVLPVLPVLPVLPV 301

DB 241 TCVSHVCAVIFVPPFGLSMWHRFSRDRSPFLPVILANILVLPVLPVLPVLPVLPV 300

QY 302 RQRILRLFHVATHASE 317

DB 301 RQRILRLFHVATHASEP 316

RN [1]

RN SEQUENCE FROM N.A.

RA RA Zhang X.; Firestein S.J.;

RT RT "The olfactory receptor gene superfamily of the mouse.";

DT RL Nat. Neurosci. 0:0-0(2002).

DT RN [2]

DT SEQUENCE FROM N.A.

RA RA Adams M.;

RA RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RA RA EMBL; AY073011; AAJ60674_1; -.

DR DR MGI:AF378854; Olfr78.

DR DR InterPro; IPR00276; GPCR_Rhodopsn.

DR DR Pfam; PF00001; 7tm_1; 1.

DR DR PROSITE; PS00237; G_PROTEIN_RECER_FL_1; UNKNOWN_1.

DR DR PROSITE; PS50262; G_PROTEIN_RECER_FL_2; 1.

RW RW Receptor.

SEQUENCE 320 AA; 35577 MW; 7161ACABF4328959 CRC64;

Query Match 60.9%; Score 989; DB 11; Length 320;

Best Local Similarity 60.1%; Pred. No. 5.3e-81;

Matches 184; Conservative 60; Mismatches 52; Indels 2; Gaps 2;

QY 8 NESSATYFILGLPGLEAAOFMLAEPGSLVLYAVGNLTIVYVTERHSLHEP 67

DB 5 NFTHAT-FILGLPGLEAFHFWGEPPLSMWAVLFNGNCIVVVFVTERHSLHEP 63

QY 68 MLCGIDILISSSMPKMAIFENSTI1QFDACILQHAFHSISGMESTVILAM 127

DB 64 MIAAIDLSTSTSWPKILAFWDSRETTDPLAOMETHTLSAESTTILLAMAFTVY 123

QY 128 AICHLRHLFVATVILPRTVKIGAVAVRGALMAPLVPVTKOLPFCRSNTLHSYH 187

DB 124 AICHLRHLFVATVILPRTVKIGAVAVRGALMAPLVPVTKOLPFCRSNTLHSYH 183

QY 188 MKLACDDIENVNVYGLVIVISAGLDSLISFSYLLIKTVGLTREQAKEF 246

DB 184 MKLAVYDTLPNVWGLTALLVMGVDWMPISLTSFLIRTVLQPLSKSERAKAFGTCVH 243

QY 247 VCAVIFVPPFGLSMWHRFSRDRSPFLPVILANILVLPVLPVLPVLPVLPVLPV 306

DB 244 ISVLAFLYPLIGLSPWHRFGNSLDPITVHLMGDYLLIPVLPVLPVLPVLPVLPV 303

QY 307 RLFWVA 312

DB 304 AMERIS 309

RESULT 3

Q8VBV9 PRELIMINARY; PRT; 320 AA.

ID Q8VBV9; AC Q8VBV9;

AC .

RESULT 4

Q8VF09 PRELIMINARY; PRT; 322 AA.

ID Q8VF09; AC Q8VF09;

AC .

DT 01-MAR-2002 (TREMBREL. 20, Created)

DT 01-MAR-2002 (TREMBREL. 20, last sequence update)

DT 01-JUN-2002 (TREMBREL. 21, Last annotation update)

DE DE Olfactory receptor MOR18-2 (prostate-specific G protein-coupled receptor Ralc).

GN GN OLFR8.

Query Match 55.5%; Score 901.5; DB 11; Length 312;
 Best Local Similarity 53.2%; Pred. No. 3.8e-73; Mismatches 81; Indels 1; gaps 1; Matches 165; Conservative 63; Mismatches 81; Indels 1; gaps 1;

QY 1 MNPDPNGNESATYFILGPGLEEAQFWLAPPCLCSLYIATVGLAVIGNLTIVYRTERHLHE 60
 Db 1 MPPGPGNGSSTSFLSISGPGLEHAWIISLPCMLCMLVLSILGNTLFTIKTEPSLHE 60
 QY 61 PMYIPLCMLSCDIDLITSSMPKLAIFWMNSTTOFACQILOMFAIHSLSGMESTVLLA 120
 Db 61 PMYFLSMLALTDGLSCLCTPLVIGIWFNGGARDISHACFTOFTIFHCLSFLESSVLL 120
 QY 121 MAFDRVAICPLRHAIVLTPRVTIGVAAVRGALMAPLWVFKOLPCRSNLHS 180
 Db 121 MAFDRVAICPLRHAIVLTPRVTIGVAAVRGALMAPLWVFKOLPCRSNLHS 180
 QY 181 YCLHODPMKLAQCDIRVNVYGLIVIISAIQGLSDLSLISFSLIILKTVGL-TREQAKA 239
 Db 181 YCLHODPMKLAQCDIRVNVYGLIVIISAIQGLSDLSLISFSLIILKTVGL-TREQAKA 239
 QY 240 FGTCVSHCNAVFVPPFPIGSMWHRFSKRDSPFLVILANLYLVPVNPVYVYKTK 299
 Db 241 LNTCVSHISAVLTFPPMIGLSVIRFGKOPHLYQWVNGEVVLLFPPVMPVIVYVTK 300
 QY 300 EIRORLRLF 309
 Db 301 QIRDRVHAHF 310

RESULT 7

Q8VGZ6 PRELIMINARY; PRT; 314 AA.
 ID Q8VGZ6
 AC 08VGZ6;
 DT 01-MAR-2002 (TREMBlre. 20, Created)
 DT 01-JUN-2002 (TREMBlre. 21, Last sequence update)
 DE Olfactory receptor MOR14-2.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV072994; AAL60657.1;
 DR InterPro; IPR012106; AATRNA_ligaseII.
 DR InterPro; IPR010064; Cystatrin.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00339; AAL_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_REC_ECF_2; 1.
 KW Receptor.
 SQ SEQUENCE. 318 AA; 35593 MW; 3A9598E821087E48 CRC64;

Query Match 54.1%; Score 877.5; DB 11; Length 318;
 Best Local Similarity 54.7%; Pred. No. 5.6e-71; Mismatches 85; Indels 1; gaps 1; Matches 169; Conservative 54; Mismatches 85; Indels 1; gaps 1;

QY 2 MNDPNGNESATYFILGPGLEEAQFWLAPPCLCSLYIATVGLAVIGNLTIVYRTERHLHE 61
 Db 1 MNDHNSQSOHIVFILGPGLEQKYMAMPLVAGVIVALEGNEVILSTIKSESSLHE 60
 QY 62 MYIFCLMSGIDILISSTSMPKLAIFWMNSTTOFACQILOMFAIHSLSGMESTVLLA 121
 Db 61 MYIFCLMSLAFADMLTCTPLSMIGLFWFNTKFTPDGCLVOMYFHTFAIESCVLLA 120
 QY 122 AEDRVVAICPLRHAIVLTPRVTIGVAAVRGALMAPLWVFKOLPCRSNLHS 181
 Db 121 AEDRVVAICPLRHAIVLTPRVTIGVAAVRGALMAPLWVFKOLPCRSNLHS 180
 QY 182 CIRQDVKLAQCDIRVNVYGLIVIISAIQGLSDLSLISFSLIILKTVGL-TREQAKA 240
 Db 181 CIRQDVKLAQCDIRVNVYGLIVIISAIQGLSDLSLISFSLIILKTVGL-TREQAKA 240
 QY 241 GTCVSHCNAVFVPPFPIGSMWHRFSKRDSPFLVILANLYLVPVNPVYVYKTK 300
 Db 241 LNTCVSHISAVLTFPPMIGLSVIRFGKOPHLYQWVNGEVVLLFPPVMPVIVYVTK 300
 QY 301 EIRORLRLF 309

RESULT 8

Q8VGZ3 PRELIMINARY; PRT; 318 AA.
 ID Q8VGZ3
 AC 08VGZ3;
 DT 01-MAR-2002 (TREMBlre. 20, Created)
 DT 01-MAR-2002 (TREMBlre. 21, Last sequence update)
 DE Olfactory receptor MOR10-2.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV072997; AAL60660.1;
 DR InterPro; IPR02106; AATRNA_ligaseII.
 DR InterPro; IPR010064; Cystatrin.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00339; AAL_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_REC_ECF_2; 1.
 KW Receptor.
 SQ SEQUENCE. 318 AA; 35593 MW; 3A9598E821087E48 CRC64;

Query Match 54.1%; Score 877.5; DB 11; Length 318;
 Best Local Similarity 54.7%; Pred. No. 5.6e-71; Mismatches 85; Indels 1; gaps 1; Matches 169; Conservative 54; Mismatches 85; Indels 1; gaps 1;

QY 5 PNGESSA-TYFILGPGLEEAQFWLAPPCLCSLYIATVGLAVIGNLTIVYRTERHLHE 62
 Db 2 PSFNESSA-TPPFVFFGIGLSHISLPCXIAIRASGSNMLVITBESSHEPM 61
 QY 63 YIFCLMSGIDILISSTSMPKLAIFWMNSTTOFACQILOMFAIHSLSGMESTVLLA 122
 Db 62 YIFLMSLAFADMLTCTPLSMIGLFWFNTKFTPDGCLVOMYFHTFAIESCVLLA 121
 QY 123 FDRVVAICPLRHAIVLTPRVTIGVAAVRGALMAPLWVFKOLPCRSNLHS 181
 Db 122 FDRVVAICPLRHAIVLTPRVTIGVAAVRGALMAPLWVFKOLPCRSNLHS 180

DR PROSITE; PS00339; AA_TRNA_LIGASE_11_2; UNKNOWN_1.
 DR PROSITE; PS0237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.

SQ 317 AA; 35357 MW; 165874EC79CAA7 CRC64;

Query Match 53.4%; Score 866.5; DB 11; Length 317;
 Best Local Similarity 53.5%; Pred. No. 5.4e-70;
 Matches 159; Conservative 58; Mismatches 79; Indels 1; Gaps 1;

Db 15 IIGLGLPGLEREAQFWLAPLPCSLXLYIAVLGNLTIVTRETEHPL 74

Db 76 ISTSSPKMLAIFWFNSTIOPDACLQMAFAHSLSGMSESVLLAMAEDRVAICHPLRH 135

Db 75 IISVTPVLPVNLVPHLHRDIEPSCILQMSLTSMEASLLAMAEDRVAICHPLRH 134

Qy 136 ATWLLPRLVTKIGVAVRGALMAALPFLPKLPPCRNSLHSCLHODPAKLAADDI 195

Db 135 TAVLTPTRIRKIGLAAVVRGMLMTLPLILKRLPPCKGVILSHCYCYPHDPLMLACPV 194

Qy 196 RYNNVVLGLIVISAGLSDLSLISFSYLILKVLVGL-TREAQAKAFCTCVSHCAYFV 254

Db 195 RYNNVVLGLIVSAGLSDLSLISFSYLILKVLVGL-TREAQAKAFCTCVSHCAYFV 254

Qy 255 VFFIGLSMWHRSKRDSPLPVTLNLYLUPPLWLPVWYKTKETRORLRLFH 311

Db 255 VPLVLVLLAHRRGTFASPLLAHTMANLFLTPVNLPLVYSLTKQIRSAVCKIKV 311

RESULT 12

Q8VGZB PRELIMINARY; PRT; 319 AA.

ID Q8VGZB; 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 21, Last annotation update)

DE Olfactory receptor MOR17-2.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID:10090; [1]

RN SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.; "The olfactory receptor gene superfamily of the mouse." Nat. Neurosci. 0:0-0(2002).

RP SEQUENCE FROM N.A.

RA Adams M.; Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.

RL Nat. Neurosci. 0:0-0(2002).

RR [2]

RP SEQUENCE FROM N.A.

RA Adams M.; Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.

DR EMBL; AY072984; AAL60647;.1;

DR InterPro; IPR00276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm_1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.

KW Receptor.

SQ 317 AA; 35851 MW; A7ABD897C708D04B CRC64;

Query Match 52.9%; Score 858; DB 11; Length 317;
 Best Local Similarity 50.3%; Pred. No. 3.1e-59;
 Matches 154; Conservative 58; Mismatches 80; Indels 4; Gaps 2;

Db 8 NESSATY--IIGLGLPGLEREAQFWLAPLPCSLXLYIAVLGNLTIVTRETEHPL 64

Db 4 NNITSTHPARLPLMGLPGLERHAWIISIPPSAYTAVLGNLTIVTRETEHPL 63

Qy 65 ELCMTCSDIDLTISSTSPKMLAIFWFNSTIOPDACLQMAFAHSLSGMSESVLLAMAEDR 124

Db 64 ELMALAAIDLWVSSSTPAPLMSLFWFDRDETFNPHACIQLQFLPSAIMESSAMLLAMAED 123

Qy 125 RYVAICHPLRHATVLLPRLVTKIGVAVRGALMAALPFLPKLPCRSILSHSYCLH 184

Db 124 RYVAICHPLRHATVLLPRLVTKIGVAVRGALMAALPFLPKLPCRSILSHSYCLH 183

Qy 185 QDVMKLAACDDDRVNVYGLIVISAGLSDLSLISFSYLILKVLVGL-TREAQAKFGTC 243

Db 184 MAVVRLACGDFPENNTIYGAVALMPLVWYKTKETRORLRLFH 243

Qy 244 VSHCAYFETVTPPEGLSMWRSRDRSPLPVILANLYLUPPLWLPVWYKTKETRORLRLFH 303

Db 1 MAPNSNSVSVSSTFVIGLPGLEEAQFWLAPLPCSLXLYIAVLGNLTIVTRETEHPL 60

Qy 62 MYFLCMLSGIDLISIISMPMLAIFWFNSTIOPDACLQMAFAHSLSGMSESVLLAMAEDR 121

Db 61 MYFLAMSLSTDAMSPLAWSLFVWLSISREIOFNICVQWMLHTSFTESSVLLAMAEDR 120

Db 304 RILRLF 309

Db 304 RYLGIF 309

RESULT 14

OBVGWO PRELIMINARY; PRT; 319 AA.

ID QVGWO PRELIMINARY; PRT; 319 AA.

AC QVGWO; PRELIMINARY; PRT; 319 AA.

DT 01-MAR-2002 (TREMBrel. 20, Created)

DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE MOR 3'BetaA (Olfactory receptor gene superfamily of the mouse.)

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RP Zhang X., Firestein S.J.; "The olfactory receptor gene superfamily of the mouse." Nat. Neurosci. 5:100-106 (2002).

RA Adams M.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY073034; RAL60697.1; -

DR InterPro; IPR00276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_1; 1.

KW Receptor.

SQ SEQUENCE 319 AA: 35988 MW; B2DB4A1465RA063F CRC64;

Query Match 52.8%; Score 857.5; DB 11; Length 319; Best Local Similarity 49.4%; Pred. No. 3.5e-69; Matches 154; Conservative 67; Mismatches 90; Indels 1; Gaps 1;

QY 1 MWDPPNGNESSATVFLIGLPGLEAQWFLAFLPCLSILKLIAVLGNLTIVYVTEHSHE 60

Db 5 IMAIASRNSSSHSTTFLIGLPGLEAQWFLAFLPCLSILKLIAVLGNLTIVYVTEHSHE 64

QY 61 PMYIFLCLMSGIDILISTSSMPKLAIFWENSTIOTFACCLQMFATHLSLSMESTVLLA 120

Db 125 MADMRYVAICFLRHSSTLSVAVGAWVNRGLAVNSPCEFMWSRMPCPKNTIPOS 184

QY 181 YCHQDVKLACDDIRVNVYGVIVISAGLDSLLTFSYVILKVKVGL TREAQAKA 239

Db 185 YCHMAYVAKLKVADTRPNRKGKLFVAVSVWGLDILIVSVYKMLRAVRLPSGEARKA 244

QY 240 FGCVSHVCAVFLYVVPFIGLSWHRFSKRDSPLPVILANITYLVPVLPNPIVYGVTK 299

Db 245 FGCVASHVGLVLYLIPALFTFLTHRFGHHVPRVHIMFANVLLVPPMLNPIIYGVTK 304

QY 300 EIQQRILRLPHV 311

Db 305 QIDRVRVGRFCV 316

RESULT 15

OBQQ07 PRELIMINARY; PRT; 319 AA.

ID OBQQ07 PRELIMINARY; PRT; 319 AA.

AC OBQQ07; PRELIMINARY; PRT; 319 AA.

DT 01-MAR-2001 (TREMBrel. 15, Created)

DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DE MOR 3'BetaA (Olfactory receptor gene superfamily of the mouse.)

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA Adams M.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY07288; RAL6051.1; -

DR InterPro; IPR00276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_RHODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.

KW Receptor.

SQ SEQUENCE 319 AA: 35979 MW; 87FFC0365FD19050A CRC64;

Query Match 52.8%; Score 856.5; DB 11; Length 319; Best Local Similarity 53.6%; Pred. No. 4.3e-69; Matches 165; Conservative 53; Mismatches 89; Indels 1; Gaps 1;

QY 2 MWDPPNGNESSATVFLIGLPGLEAQWFLAFLPCLSILKLIAVLGNLTIVYVTEHSHEP 61

Db 1 MATNSNSPTTSSVFLIGLPGYFHSWISPRCPKNTIPOS 124

QY 62 PMYIFLCLMSGIDILISTSSMPKLAIFWENSTIOTFACCLQMFATHLSLSMESTVLLA 120

Db 61 MYFLFLAMSLSTDMASLPTTMSLFRVMSISREIQFNICVWQMLHIFPTESSVLLA 120

QY 122 AEDRYVATCPLRHTVTLPLPRTKIGVAVVARGAALMAPLWIKLPCNSNLHSY 181

Db 121 ALDRYVATCPLRHTVTLPLPRTKIGVAVVARGAALMAPLWIKLPCNSNLHSY 180

QY 182 CLHQDVKLACDDIRVNVYGVIVISAGLDSLLTFSYVILKVKVGL TREAQAKA 240

Db 181 CLHQDVKLACDDIRVNVYGVIVLWGLTILWGLMSLGVIVSVILHSLVKLASREGKAL 240

QY 241 GTCVSHVCAVFLYVVPFIGLSWHRFSKRDSPLPVILANITYLVPVLPNPIVYGVTK 300

Db 241 NTGASHICAVLILYVPMGLSIVHRFAKHSPLHIFAHYLLVPPVLPNPIIYGVTK 300

QY 301 IROIRL 308

Db 301 IREGILHL 308

Search completed: March 26, 2003, 09:55:37

Job time : 89 secs